STIC-Biotech/ChemLib

From:

Sent:

Slobodyansky, Elizabeth Wednesday, July 31, 2002 11:44 AM STIC-Biotech/ChemLib 09/900,038

To: Subject:

Please search for case 09/900,038:

SEQ ID NOs: 1 and 2 against commercial and interference databases.

Thank you.

Elizabeth Slobodyansky, PhD

Primary Examiner

Art Unit 1652 CM1 10D11 703-306-3222

mail box 10C01

Point of Conta
Searcher: P Sheppard
Searcher: Sheppard Phone: 7703) 308-4499 Location:
Location:
Date Picked Up:
Date Picked Up: Date Completed: 8/6/02
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

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Streptococcus agalactiae DNA. Streptococcus agalactiae Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae; BCT 03-FEB-2001 2. (bases 1 to 9987)
Miyake,K., Watanabe,M. and Iijima,S.
Direct Submission
Submitted (01-NOV-2000) Katsuhide Miyake, Nagoya University, Grad.
Sch. of Engineering, Dept. of Biotechnology; Chikusa-ku, Furo-cho, Nagoya, Aichi 464-8603, Japan Streptococcus agalactiae cps1bb, cps1bF, cps1bL, cps1bL, cps1bL, cps1bJ, cps1bJ, cps1bJ, cps1bJ, cps1bJ, cps1bJ, cps1bJ, cps1bJ, cps1bJ, neuB, neuC genes, complete cds. AB050723 shows Miyake,K., Watanabe,M. and Iijima,S. Opsy of Streptococcus agalactiae type Ib beta-1,3-galactosyltransferase activity Unpublished Streptococcus. (sites) REFERENCE AUTHORS TITLE JOURNAL JOURNAL

Description

SUMMARIES

Query Match Length DB

Score

Result ۶ 9

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AB008676 AC079621

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(E-mail:miyake@proc.nubio.nagoya-u.ac.jp, Tel:81-52-789-4278,
Fax:81-52-789-3221)
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LEFLISTDMEIYK PSGEITNLPY LEKIGKOQKK VILSTGMAVMEEIHQAVNILRQNG
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Pred. No. 2.5e-134;
0; Mismatches 0;
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gattatgattttgcaataagaggagctctggctgatttcaaaatcggcttactcaataaa
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Submitted (19-JAN-2001) Infectious Disease, Immunology & Submitted (19-JAN-2001) Infectious Disease, Immunology & Rheumatology, Children's Hospital and Regional Medical (Sand Point Way NE, Seattle, WA 98105, USA Location/Qualifiers 1..164448 | 1..164448 | Archiver Archive Arc
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McKinnon, K., Chaffin, D.O. and Rubens, C.E.
Direct Submission
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919. .924
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Sult.c.J., White,O., Olsen,G.J., Zhou,L., Fleischmann,R.D., Sutton,G.G., Blake,J.A., FitzGerald,L.M., Clayton,R.A., Gocayne,J.D., Kerlavage,A.R., Dougherty,B.A., Tomb,J., Adams,M.D., Raich,C.I., Overbeek, R., Kirkness,E.F., Weinstock,K.G., Merrick,J.W., Glodek,A., Soctt,J.D., Geoghagen,N.S., Weidman,J.F., Fuhrmann,J.L., Nguyen,D.T., Utterback,T., Kelley,J.M., Roberts,K.M., Kaine,B.B., Borodovsky,M., Klenk,H.P., Fraser,C.M., Smith,H.O., Wocse,C.R. and Venter,J.C.
Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii

Science 273 (5278), 1058-1073 (1996)
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Bult.C.J., White, O., Olsen, G.J., Zhou, L., Fleischmann, R.D.,
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Peterson, J.D., Sadow, P.W., Hanna, M.C., Cotton, M.D., Hurst, M.A.,
Roberts, K.M., Kaine, B.B., Borcodovsky, M., Klenk, H.P., Fraser, C.M.,
Smith, H.O., Woese, C.R. and Venter, J.C.
Direct Submission
Submitted (27-Aug-1996) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
On Jan 30, 1998 this sequence version replaced gi:1591709.
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YLSRIKKQKLYSYTLKTHWKNKKHFCNNVYFWKVFFYSLVVYLFIVLFPFILKILI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation-"MKIIGIIQARTGSKRLKNKVLLKLGDRCILEILLERLKKSKKLD
DIIVATTIKEDNAIVELONGLGVNVFRGSERDVLDREYNASKEYSGDVIVRITGDNP
LISIELIDKQVEYLLKNNFDYVSTKNIILGISSEVFTFDALEKAWKNAKEKYQREHVT
PYIVENPULKKVFYLEPPEYLKRGIRLTIDTIKDFKYLELGKHFDLINVDIRQIID
FLDKNPQIKNINSNVRQKSYREVEE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
/product="spore coat polysaccharide biosynthesis protein F
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HYDFK HIRKYDSSTIIKSGTLLRPVEIAARGMKIIGBENFGEPYVENVPEBEGI
LEIGDNCGIGSFSIINATKKITIGSNVLISHYNIIDGDHGFKRGELIRNQKNYSEPI
EIGDDVWIGTGVKILKGVKIGEGAVIGAGSVVTRDIPPYSVAVGVPARVIKKE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MKIAIITDGSVEMCMCHVYRTLSLANELRKFNVNEIIFFTKSDE
DVIKKIEENGFKVIKCSDNNDILKNIKNIKPDVVIIDDLGIEEDFAKNIRELCKKLIF
FDNPNPSSNKYADIVVNAIVGSELKNRKYFDEENKTLYFYGPKYLILRNEFYKVKKEM
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                                                                                                                                                                                                                                                                 /note="similar to GB:X73124 SP:P39627 PID:413993 pe identity: 32.60; identified by sequence similarity; putative"
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/note="similar to GB:X73124 SP:P39626 PID:413992
GB:AL009126 percent identity: 38.94; identified be
sequence similarity; putative"
/codon_start="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="MJ1065"
/note="similar to GB:X73124 SP:P39625 PID:413991
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/protein_id="AAB99067.1"
/db_xref="GI:1591716"
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/protein_id="AAB99065.1"
/db_xref="GI:1591714"
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/db_xref="GI:1591715"
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                                                                                                                                                       complement(6752. .8206)
/gene="MJ1062"
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/gene="MJ1064"
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                                                                                                                                                                                                                          complement(6752. .8206)
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/transl_table=11
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Best Local Similarity
Matches 365; Conserv
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SNCFVFSSLWEGLPNTVIEALSLNLPVISTCCKTGPREILCPELNISDKIDPPYGKY
GILTRPFSREFIWQDLNEKPLIEEEKMLADLMIKMIEDEDLRKRYSNGLERAKDFDIE
KIIKEWKLLIEGTI"
                                                                                                                                                                                                                                                                                                                                                                                                                                        KIQRLAMAGGVVANVIMNLNIFERTPFEELYIFPAMGDDĞVAAGAAILKAVELGEDIS
WLKDLEMPYKGPNYSREDVRELKKDKWKDKITYEYIGEKWPEIAARKIAKINIJAVY
WGKMEFGPRALGNRSILADPRDPKTRDK INSTVKRPWFQPFCPSVLEEERERLFEKS
YKHKHMAIAPERMKEFWDKLPSAMHIDGTARPQFVEEKDNPNYYRLLKKFKEITGYGI
VINTSFNLHGRIIVRTPEDAITDFIDCNIDAMFIEGYLVKRKI"
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YNFINLPKYIKDYYKKRQDYLFIEDILNLKLGFDILLNSSKIFKKVNLTNYNDEHEKF
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FELYWKKYPKKEKTILLPGSGYPEFFERESEIKNFRDKKLINTLEHGYSFFKRHFGEY
INDFSIRELEKLKNIKEIK INGLNEVPEYTIGMSSTMIYELLNAGSKSFFLESNAKE
TFMMDDKEFKKYFRKNLKEIFFEILNKQL"
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protein_id="AAB99064.1"
/db_xref="GI:1591713"
/translation="MPQDISNPYKDKTILVTGGTGSIGKEIVKTLLKFNPKTIRVLDI
                                                                                                                                                                                                                                                 /translation="MVKILGVKYFLHDSGVFYIDTKNKEIFGILTERVTRIKHDGGTV
IPILNEYPKLKNIDYVAYPFEGTNLDFILFKHIDDYIKRTYKPKYIKEYAKYKKELSQ
NKTKFVLNNIYRPFIWEILAVYGLRKLLFKRFNNIYNKLGNLAIKRELKKIFRKDVSL
                                                                                                                                                                                                                                                                                                                                                    YEHHLCHAASAYYFSPFFPKETLVFTLDGIGDWKYHSLWLFKEYDYRLVSYSSFDIIC
                                                                                                                                                                                                                                                                                                                                                                              YDDVEGIFKGASIGHIYSLFTEILGFTPNSDEGKTEALAAYGKPNGELYNLLKKGYKI
NKEKLRWEHDINILKKLHNKQYLQKWKEKIGDENFAATIQRWLEDTVVEYLNIVYEKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MSNKKKOLTVMGTVWDFWSVLKMFDKLYESKYISFYEPWLKGEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DKEKIILFNEKSKNPLLWPFKILKRTYKILKIIREFKPDLVITHHDDANVSIIPVILL
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ESHFKSLKNKTKIVPNVYEIDKLOOLSNEPLEKOYRNIFKDSFVFINIGRLTEOKGOM
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SYKNNKFIKKDEFEHLVYNTFLYFLINWDNLYHTNQMPFYIWYNFKERVDDILKSEKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to GB:U10927 SP:P39862 PID:506709 percent identity: 31.91; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product-"capsular polysaccharide biosynthsis protein M"
/protein_id="AAB99063.1"
/db_xref-"GI:1591712"
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/protein_id="AAB99072.1"
                                   /note="similar to PID:1653353 percent identity: 35.19; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4130. .5743 /
/gene="MJ1060"
/note="hypothetical protein; identified by GeneMark;
putative"
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by sequence similarity;
                                                                                                                                                          /product="nodulation protein"
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                                                                                                                                                                                       /protein_id="AAB99062.1"
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/gene="MJ1061"
complement(5738. .6739)
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putative"
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/transl_table=11
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4130. 5715
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/gene="MJ1059"
2913. .4133
/gene="MJ1059"
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                                'note="similar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteroides fragilis NCTC9343 Produces at Least Three Distinct Capsular Polysaccharides: Cloning, Characterization, and Reassignment of Polysaccharide B and C Biosynthesis Loci Infect. Immun. 68 (11), 6176-6181 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 (bases 8470 to 34508)
Coyne, M.J. and Comstock, L.E.
Direct Submission
Submitted (07-JUL-2000) Channing Laboratory, Brigham & Women's
                               257 atatttttagaatggatgctgatgatatttcatatccaagtagatttgataagcaaattc 316
                                                                                                                                                                                                                                                                                                                                                                       581 AAAATGGAATAT-----TTTAAAAGAGTTTAAACCCAGAAAATATAAATTTAAAGAAA 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A Conserved Region of the Bacteroides fragilis Chromosome Upstof the Polysaccharide B Locus Contains Genes Implicated in the
221 TAATGGCAACATACAACGAACCAGAAAAATATTTAAAGGAATCTATTGAGTCAATTTYAA 280
                                                                                                                                                                                                    AAAGAAATTTAGGTAGAGGAGCCAGTAGAAATAAAGCTGTTAATATATAGCAAGGGGGAAGT 460
                                                                                                                                                                                                                                                                                                       317 gttttatggaggaaaattca---ttggatttctcagcaactctaatagaattgatagacc 373
                                                                                                                                                                                                                                                                                                                                       521 AATATATGGAAAATAATAGAGACATTGATTTATTGTTTAGCTGGGTTTATTTTTTTGATG 580
                                                                                                                                                                                                                                                                                                                                                                                                                                              aagttttcgataagttaatgggatatagagatttagtacctgttgaagattatgattttg 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAATCTTAAAGAAATTAAAATACGATGAGAAATTAATTAGGTCTCAAGACTACGATTTTT 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 caataagaagagctctggctgatttcaaaatcggcttactcaataaagtacttttacagt 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               755 GGATTAGATGTATAGCCAATGATTACAAATTTGACATAATTGAGGAATTTTTATTAAAAT 814
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Bacteroides fragilis NCTC 9343 PS B capsular polysaccharide
                                                                                                 taaagcaattottaacagaatattoagttgtagataatagaataaaaatottgottaatg
                                                                                                                                                                    aagaaaatattggtttagcatcaagtttgaacaaagcggtgaaaatttctaagggagaat
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Coyne, M.J., Kalka-Moll, W., Tzianabos, A.O., Kasper, D.L. and
Comstock, L.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atagattaaacgagaatggaatatcacaaaaccaataagtttaagcaatatttactc
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Coyne, M.J. and Comstock, L.E.
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Bacteroides fragilis
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/procedi_d(="Abadis00.")
//db_xref="G1:18152890"
//db_xref="G1:1815890"
//db_xre
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IEEESGIRKOKIAVCGNESSHWOYFFLATLYYGAYIVPLILEERADNYNINNHSEA
KILFYGDVYWENLINESAMPLLEGILMMUNDFTLLVSREERLTHAREHINEMEGKFFPKN
FRKEHIETHKDQPEELAVINYTSGTTSYSKGVMLPYRSLWSNNAFAFEVLPLKAGDKI
YSMLDYMAHWYGLAFEFLYEFAVGQYTTRYRNESPKIIGFAFDVKPKLIAVPLIE
KIIKKSYLPKLETPRYKLLKPPIINDKIKATVREENIKGFGGNFEAVIVGGAAFNOE
VEGFLRMIDFPYTVGYGWTEGGPIICYEDWKRFKFGSGGRFEAVINGSVAFNOE
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SNVNGNNLAGLSVSGLVNITGNKAKGVLITGLSNIAGDNMRGLMMSGIMNITGDKAAG
VQLAGLANTYGEBYDGLMMSGLLNVVGEBMNGLQLSGLANTYGGQMNGVQLGLFNFAS
KKGLQIGLFNYKKEDMKGLQLGLVNNYGFBMNGTVQCGNTKINVGARFKNKLYT
ILGGGTHYLDPDDKFSAALFYRAGLEDLYRNLFVSGGNSTKINVGARFKNKLYT
LYALQARLNLEYRFGFREGLEDLYRNLFVSGGISQOH ETFRNKKVBGIPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAL61888.1"
/db_xref="GI:18152897"
/translation="MKKIILVAALLSAAVCLPAQNKGGNKSGGINLSLWKKACTQPLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEIVCKGPNVMLGYYKNEEATAQVIDKDGWLHTGDLALEDAEGNITIKGRSKNMLLSA
SGONIYPEEIEDKLNNLPYVAESIIVQONDKLVGLVYPDFDEAFAHGLKNEDMERVME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(222. .1379)
/note="Orfl; Glycine- and asparagine-rich protein with a large number of clustered repeats; similar to putative pentose-5-phosphate 3-epimerase (PPE) protein from Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                     181 Longwood Avenue, Boston, MA
                                                                                                                                                                                                                                                           Laboratory, Brigham & Women's
          Boston,
                                                                                                                                                                                                                                                                                                                                                                                                   update by submitter
, 2002 this sequence version replaced gi:11023503.
Location/Qualifiers
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COMDIEMENT (3340. .4422)
/gene="fc1"
Hospital/Harvard Medical School, 181 Longwood Avenue,
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/product="GDP-4-keto-6-deoxy-D-mannose-3,
5-epimerase-4-reductase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fragilis"
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/rransl_table=11
/product="unknown
/protein_id="AAL61889.1"
/db_xref="GI:18152898"
                                                                                                                                                                                            Direct Submission
Submitted (16-MAR-2001) Channing
Hospital/Harvard Medical School,
02115, USA
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/organism="Bacteroides
/strain="NCTC 9343"
/db_xref="taxon:817"
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                                                                                                                                                  Comstock, L.
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/transl_table=11
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                                               02115, USA
4 (bases 1 to 34508)
Coyne, M.J. and Comsto
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VMDNLHVSEYWMPFTTGLLVYPVMLLCSWLLNOIPAPNEQDIIQRTKRAPMDGKDRRK
FLROFFWGICMLVVFYGALTYPRELADSFAADIWKELHIEGAMIFTOTEVPIAAFVLV
IMELIVFVRNNRLALNIIYCLAVTGGSLMVFSTLLYVGFLSPIWWMILSGLGLYMGY
IPFTYLIERLIASHYVSTAVFIIXTADSFGYLGTTGVFMVKNFVSADISWTVMLMRT
ALFSGFVSVLSIFAIXCYFKQQLNSLLIPSEHD"
                                                                                                                                                                                                           /translation="MIRSFLSRSPLYVLALYASVLIFLYYTCAYAYRRPFTAA1YEGE
ILWGFDVKILYVLSEIIGYALSKFIGVRILPSMKAGHRIYYIIGLLTFSBVALLGFAL
LPVPLKVCSIFLSGLPLGMIWGVIFSYIEGRRISEILNVGLSVALIVSSGLVKTLGQF
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Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Clostridium.
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Nolling,J., Breton,G., Omelchenko,M.V., Markarova,K.S., Zeng,Q.,
Gibson,R., Lee,H.M., Dubois,J., Qiu,D., Hitti,J., Wolf,Y.I.,
Tatusov,R.L., Sabathe,F., Doucette-Stamm,L., Soucaille,P.,
Daly,M.J., Bennett,G.N., Koonin,E.V. and Smith,D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22262 AAGATTAGCGTATTGATGTCTATATAAAGAGAATTCTCTTTATGTAAGACAAGCTATT 22321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22382 GAAGATTTATTTAGATAAGTTAGTTTTAGAAATAGCAAGAAAAGATAGTGGTATACAA 22441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22442 TATCAACGAAATGAAAAAATATAGGTTTAGCAGCCACTTTGAATCGTCAGATTTGTGTA 22501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 agtagaggtgatttaaagcaattcttaacagaatattcagttgtagataatagaataaaa 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 gaatctatattaaatcaaacgcttactgattttgagttcataattgtcattgataatcca 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative glucose-1-P-cytidylyltransferase"
/protein_id="AAG26464.1"
/db_xref="G1:11023507"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clostridium acetobutylicum ATCC824 section 205 of 356 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 aattatagtatcattatgtcggtatatataatgagcctttaaattatgtgagagattcagta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 120.8; DB 1;
Pred. No. 5.8e-10;
0; Mismatches 132;
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                                                                                                                                                                /protein_id="AAG26463.1"
/db_xref="GI:11023506"
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                                                                                                                                            /product="unknown"
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Clostridium acetobutylicum.
                                                                                                                     /transl_table=11
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AE007717 AE001437
AE007717.1 GI:15025159
                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="wcfU"
11754. .12473
/gene="wcfU"
                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                         11754. .12473
                                             .11761
                                                                 /gene="wcfT"
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60.2%;
               /gene="wcfT'
10478. 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 12.9°
Best Local Similarity 60.2°
Matches 200; Conservative
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E"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YVSFEIFPFSFSEHRILERVEATGKNYAEYMGKGALDILENLDDAEAGWKAEGALDILERULDDAEAGWKAEGALDILERULDDAEAGWKAEGALDILERULDDAEAGWKAEGALDILERULDDAEAGWKAEGALDAETILERULDDAEAGWKESYDTVANYI ILYPETBYRIRHYBYQIRSKETLLGSCKYYINDWSFWRHLYPFFAGSRKSCFENGVYL ELRRAGYTVFYGYAEGGKLVDFVGKKCDRIYYLQCAPLLNDFGVEGWKYTLEMIQDN YEKWVVSMDDTTLESKEGIRHIQVWQLPEIL"
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complement(8120. .8467)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RQLKYRRKRVEVPVIKNLIFIQATKQDACDÏSNKYNIQLFYMKDLLTRAMLIVPDKQM
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9468. .9992
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/gene="upb2"
9996. .10481
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/gene="upby"
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EELEKEVTARIPIRTNRDDRYFTNYVOGLPLOGYTKNFENMLNHENIHIMLNTDYKFI
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complement(6689. .8038)
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complement(5661..6560)
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2 (bases 1 to 14157)
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6 (childress, base 1 to 14157)
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7 (childress, base 1 to 141
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COMPLEMENT(1268 . 2119)
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complement(1268 . 2119)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="Nucleoside-diphosphate-sugar epimerase"
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Bacteriol. 183 (16), 4823-4838 (2001)
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complement(2227. .3963)
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1 (bases 1 to 3584)
van Der Well, H., Morris, H.R., Panico, M., Paxton, T., North, S.J.,
Dell, A., Thomson, J.M. and West, C.M.
A Non-Golgi alpha 1, 2-Fucosyltransferase That Modifies Skpl in the cytoplasm of Dictyostelium
J. Biol. Chem. 276 (36), 33952-33963 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF279134 3584 bp DNA linear INV 05-SEP-20 Dictyostellum discoideum alphal, 2-fucosyltransferase (fucB) gene, complete cds; and unknown genes.
8638 ATTTATGATGATAATAGAGAAAAATATTAAATTATTGGTATTGTTTAGCACACATCCTTCA 8579
                                                                                                                                                                                                                                                                                                                                                                                                                                                               8341 AAGAAAGACTTTAAATACATAGTATGGGGTGCAAGTAATGGAGGCAAAATTACAAAAGAG 8282
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                                                                                                                                                    gaagattatgattttgcaataagaggagctctggctgatttcaaaaatcggcttactcaat 597
                                                                                                                                                                                                                                                                 caatattttactcagctattttacaagatttttataaagaaaaatcttatattgatatc
                                                                                                                                                                                                                                                                                                                                                                        8401 TATGAAGGTTTAAAAGATGGAATAAAAATAAAATTAATAGATGTTTTTAAGAGAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                    acaaaaattactaattactttcaagagtatgtgataaagaaacgctatactcagcaagag
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                                                                                                                                                                                                                                        aaagtacttttacagtatagattaaacgagaatggaatatcacaaaaccaataagtttaag
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                                                               tggtgcgtaaaaaaaaaagttttcgataagttaatgggatatagagatttagtacctgtt
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van der Wel, H. and West, C.M.
Direct Submission
Submitted (15-JUN-2000) Anatom
Florida College of Medicine, 1
32610-0235, USA
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EVENKNKDVDILACKYVEAFGDVSREGKLEREHWYNVDLNNSESIESLFLENCYIAHPS
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                                                                                                                                                                                                                                      GFIDKYKEGEVDECRIYKPEDLMKLHSDYVFIATLPGKEEADEFLKNCGLKKFKEYIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation-"MISVIMPVYNCEKYLEESIESILKQTYRDFEFIIVNDGSNDKSI
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Extremophiles 3 (3), 227-233 (1999)
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HORIKOSHI, K. TSUJII;
249-284; Springer-Verlag (1999)
(sites)
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halodurans genomic DNA,
BA000004
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Extremophiles 3 (1), 29-34
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8 (sites)
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Takami,H. and Horikoshi,K.
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Bacillus halodurans
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Bacillus halodurans genc
AP001519 BA000004
AP001519.1 GI:10176109
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IERLUKEAIQKDQELNQVKKIAEABRSRLCLLKDKYKEVRNELIEKELVK"
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/db_xref="GI:9022427"
/translation="DPTKENNTVGHVVKQGYRLHDRLVRPAMVGVNKIKPQ"
442 c 365 g 1290 t
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                                                                                                                 /product="alphal,2-fucosyltransferase"
<1067. ..>3373
/gene="fucB"
1067. ..3373
                                                                                                                                                                                                                                                                                  /codon_start=1
/product="alphal,2-fucosyltransferase"
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/db_xref="GI:9022426"
                                                                                                                                                                                                                                                           /note="glycosyltransferase
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/gene="fucB"
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Makasone,K., Hirama,C., Takaki,Y., Masul,N., Fujl,F.,
Nakamura,Y. and Inoue,A.
An improved physical and genetic map of the genome of alkaliphillic
Bacillus sp. C-125
Extremophiles 3 (1), 21-28 (1999)
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Masui, N., Fuji, F., Takaki, Y., Inoue, A. and Horikoshi, K.
Sequencing of three lambda clones from the genome of alkaliphilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence analysis of a 32-kb region including the major ribosomal protein gene clusters from alkaliphilic Bacillus sp. strain C-125 Biosci. Biotechnol. Biochem. 63 (2), 452-455 (1999)
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Takami,H.
Genome analysis of facultatively alkalihilic Bacillus halodurans
                                      1589 TCTTTTAAATTTTTCAACATCCTGATAAAGATATTTTAATGTGGTCAATGTTTTTCAAT 1648
aaaatatacttaactaatgatatacggaagatgttattgaatagatctatacttgcccac 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takami, H. and Horikoshi, K. Reidentification of facultatively alkaliphilic Bacillus sp. to Bacillus halodurans
Biosci. Biotechnol. Biochem. 63, 943-945 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 (sites)
Takami, H., Masui, N., Nakasone, K. and Horikoshi, K.
Replication origin region of the chromosome of alkaliphilic Bacillus halodurans C-125
Biosci. Biotechnol. Biochem. 63 (6), 1134-1137 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetic analysis of the chromosome of alkaliphilic Bacillus halodurans C-125
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Takami,H., Takaki,Y., Nakasone,K., Hirama,C., Inoue,A. and
Horikoshi,K.
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Bacillus/Staphylococcus group; Bacillus.
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Takami, H., Takaki, Y., Nakasone, K., Sakiyama, T.,
Sacaki. R., Hirama, C., Fuji, F. and Masul, N.
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/protein_id="BAB07209.1"
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NEASHQQLYQDIFTACQEAQDCQRQLYELMFKKGWYSLEAAPEQKLQEAYQQFSGYMN
QLPYH"
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/translation="MNYTRDSRPLFQQVADAIANDIIHNVIKEGEQVPSTNQFAKHH
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                                                                                                                                                                                                                           EQRKGLTLEDRAVRNRLÄTLALKKLÖKOKPAPLSRKSHVHYTOPGNLEDDVEKLAEVD
WITEVVVENLDVKKOLFEKVDOYRKOGTLVSSNTSGISIEAMAKGRSEDFQAHFLGTH
FFNPPRYLKLLEITPFKKTKPEVTAFWKAFAEDVLGKGVVEGKDTPNFIANRIGTYGL
                                                                                                                                                                                                                                                                                                          LUTVQKMLEGGYSVGEVDSVTGPLIGRPKSATFRTLDVVGLDTFLHVAKNVHDVVDGE
EVDVDPPPVPKKMARDRQMIGSKSQGOFFLKQKGRGSBILEHRSTLEHSSTLETSFKRKMKA
PSIEDAKQAKSLNELSILIGADVALSOGFFLKQKGRGSBILTSPRSKYVETAGDIRAVDDA
MKWGFGWEOGPFEMWDAIGVASSVQRWEEEGATVPSWVKEMLTSGRERFYQDGTFYHH
GEKVIPINKALHLKALKPRVTIKNSGASILDGDDVALLEFHSPNNSIGFDVVQM
INKAVDEVENYYTYJGNGFRFVTRNSGASILDGLDDVALLEFHSPNNSIGFDVVQM
INKAVDEVENYYTYJGNGFRFVTRNSGASILDGLDVALLEFHSPNNSIGFDQQAMAK
IRRAVDGANYKGYJGNGGFEICLPTASIQASIGTYMGLVEVGVGVIPGGGGNKELY
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YQAKQQVIHLHDAGYRPPARKKIPVVGETGYATMLLGAKSMKFGGMISEHDLKIAEKL
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Abaxxef="cd:10176113"
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AHFFAQQCQDPEVKQALEQAGQMHQRHYTMLGHLQNQQNMATVQ"
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                                                                                                                                                                                                /translation="MARQIRKVAVIGSGVMGSGIAAHLANVGIPSLLLDIVPNQLTEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AFVIAGGRVAKGTLVDEQYLLDLEREAFLSLVGEPKSQQRMQHMLMKGKPLRN"
                                                        /transl_table=11
/product="3-hydroxyacyl-CoA dehydrogenase/enoyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="transcriptional regulator (GntR family)"
/protein_id="BAB07211.1"
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5746. .6015
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GLSEDQNCGREVAKAIAEYAIGESLNKVVGSEALDFVADENVQIHGGYGFMAEYEVE
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RTEKAIRRGLEKAAEQKLALTQVFCQGAFNRIEAHAKESLVAMGSGDTLRTWTSILRK
                                                                                                          9 (sites)
Nakasone,K., Masui,N., Takaki,Y., Sasaki,R., Maeno,G., Sakiyama,T.,
Hirama,C., Fuji,F. and Takami,H.
Characterization and comparative study of the rrn operons of
alkaliphilic Bacillus halodurans C-125
Extremophiles 4 (4), 209-214 (2000)
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VSREDQDAFAVESHKRAAKAIEEGKFADEIVPVDVTLGHVDDHKLVBEHVTFSVDEG
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SFAVAGVAPEIMGVGPVEAIPKAVKMAGLDLSDIGLFELNEAFASQAIQVIRGLNLDH
DKVNVNGGAIALGHPLGCTGTKLTLSLIHEMKRRGEQFGVVTMCIGGGMGAAGVFELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (22-MAR-2000) Hideto Takami, Japan Marine Science and Technology Center, Deep-sea Microorganisms Research Group: 2-15 Natsushima, Yokosuka, Kanagawa 237-0061, Japan (E-mail:takamih@jamstec.go.jp, jp, URL:http://www.jamstec.go.jp, jp, Tal:81-468-67-3895, Fax:81-468-66-6364)
                                                                                                                                                                                                                                                                                                     Takami,H., Nakasone,K., Takaki,Y., Maeno,G., Sasaki,R., Masui,N., Fuji,F., Hirama,C., Nakamura,Y., Ogasawara,N., Kuhara,S. and Horikoshi,K.
Complete genome sequence of the alkaliphilic bacterium Bacillus harddurans and genomic sequence comparison with Bacillus subtilis Nucleic Acids Res. 28 (21), 4317-4331 (2000)
Analysis of the genome of an alkaliphilic Bacillus strain from an
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                          industrial point of view Extremophiles 4 (2), 99-108 (2000)
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complement(1909. .3090)
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complement(3111. .5492)
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Takami, H. and Takaki, Y.
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Submitted (24-SEP-1998) P.falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
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On Dec 16, 1999 this sequence version replaced gi:5763807.
On Dec 16, 1999 this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the
                                                                                     246029 AAATTATTTAAGCGAAAGTATAGAAAGTATCCTAAACCAAACATTGBAAAACTTTGAGTT 245970
                                                                                                                                                                          245969 TCTAATAATGATGCTTCTACTGATGGAAGTGG---GGAATTCCTAGAGTACTC 245913
                                                                                                                                                                                                                                                 245912 AAAGAAGGATAAACGAATAAATTCACAATAAAAAAAAATAGAGGTCTAAGTTACAG 245853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245558 TAATCTAAGACGCCGTCAAGATTATGATCTATGGTTTCGCTGCTTAGAAGCCAAACTCAA 245499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
I (bases 1 to 67970)
Bowman, S., Churcher, C., Harris, B., Harris, D., Lawson, D., Quail, M. and Barrell, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                  245792 TGTTTCATTTAAAGACCGTCTTGCTGTTCAAATGGATCATGTTAAGGCCCACTCA--GAA 245735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245734 CTCGATATACTTGCTAGTTATGTTATTGATATAGATGATAAAGGGAATGAGTTGGAAATA 245675
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                                                                                                                                                                                                                                                                                                                   281
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                                            aaattatgtgagagattcagtagaatctatattaaatcaaacgcttactgattttgagtt 101
                                                                                                                                    cataattgtcattgataatccaagtagaggtgatttaaagcaattcttaacagaatattc 161
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  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245674 AGAAAGGTACCAACTACACATAA----GAGATTGCTAATTTAATATGGACTTGCCCTTT
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Mismatches 281; Indels
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1. .67970
/organism="Plasmodium falciparum"
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/strain="3D7"

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IIAKKEYEEFIKYFKNEQVENSKMENGNKKICDGEKDNNNLMEILLEKNLDTIPGFKY
NEKDKEYLENLKKKIIKYPNRIVCIGEIGLDFDRLYFCSKYIQIKYFIFQLKLVQMFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPMFLHMRNCSETFFKIVDIYKFLFEKNGGVIHSFTDKEDIVHIIVQNYÄNLYIGVNG
CSLKSLENINAVKKIPLNLLLETDAPWCGVKKTHASYEYIKDTYEKRAYTNLKKIKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMRKLLSGETNSTKLDNGDELKIKLNDEKHKDSTKWDKSYSFISNLEEEKYSQTDLFR
KKQEINEANTKIIEDRQEFYILNNDEIENIATRFVLENNFDELYIQSFKQSLIDIIQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MTTYRENVGISNKGNKKKKSCQNISFLNFLSFDWIRPLINDLIK
GDIQELPNICRNFDVPYYASKLEENLRDIEVEDSEFYSEKNSSNEHVLHHCNSNDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKVYNYYYHNILMSILKTFKFRIILISFYILFTLIVTLGGKFIDYYMRILEGQKIPV
YISFLKDFKVFSGLVVVMIMFFHLFFEALLHFYFHLFTINLKVSLMYFLYKINLCSNN
NHLQNPDAFYNTYRKFSSQTEIDEISRDFLSIGKNASSSSSGIKNNNKNIDNNKFVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DYIINFIKSTKKMEKDSLNENRSLPNVNIYNIMFSDVPSVTFFYTSCINLFNVFVKIF
MSFYVFHIKIGSNSVGIAIMLSIALYSAMILFEFLPSLFKSKYLIYRDKRIDNMHHVL
KEFKLIKMFNWESFAFKYINIFRMKEMKYCKIRLYLSNIGVFISSISSDIVEVVIFFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MKLLNNRFVVLCPIIILFFFLNSVVLGNNNRNNINFHETENAAK
                                                                                                                                                                                                                                   aa
                                                                                                                                                                                                                                                                                                                     /product="conserved hypothetical protein, UPF0006 family"
/protein_id="CAB63556.1"
/db_xref="G1:6594244"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8020. .10389
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/gene="MALIP3.03"
/gene="MALIP3.03"
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      .3276))
                                                                   .3276))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence, atg/gttaaa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="potential splice donor sequence, aaa/gtaaaa"
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      .2598,2748. .2848,2990.
                                                                   .2598,2748. .2848,2990.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="potential splice acceptor sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative ABC transporter"
/protein_id="CAB63558.1"
/db_xref="G1:6594246"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MAL1P3.02, hypothetical pro
contains possible signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="potential splice donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(2599. .2610)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(2742. .2747)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(2984. .2989)
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complement(join(1748.
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complement(join(1748.
/gene="MALIP3.01"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IIKCDDNTIFKERNEPYNIA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5005. .5496
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HDKEFITTHWIKMIQDEDIEFFLNLQVFWLRILTLELFYKNKE"
complement(32477. .32486)
/gene="MALIP3.04"
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IANEVLKNIHSFTNIENIFSLINDSSKSPVLKTFLKEFGSIFPHMLNNVPKLLFDLCQ
                                                                                                                                                      YTLDTYTSNNSDKEEIVKPLYKDTHEEFNKSSSMPFVKSSSNMINNPSNFKYEDNSSS
FKGSISLETTLWYFQQVGFVLLTSVVIFMLISIFTDEIKFVFLTMMSIISKNNKEHSD
TILOKQVRYEDFYVLEDIISLYTSGICFSMIIYGNITSAIKVHNNILYSILNAPLYIF
YNNLGNIINRFIIDISAFDYFFLKRIYKAFFIFFCILSSLLIIYMINDCIFIFPFV
ILLIYFFVFRRPSGCKRAPQRLKRIYKAFFIFFCILSSLLIIYKKNTYHLDVYF
HYINNFRISYFFKRPSGCKRAPLINIMASLYIKIFLLLTTYIIMHPHLYASGIIKLYKEKNYVRI
                                                        TLÖNPL.I EDILLDNVQY EVNI PEIQDKTLKY RGNI SEYMEKNNLNITK ESHWGY SNLNT
I DYTRIK LFDEVELNHVKHSNKMIYKEAY FVKGNTESVSFEIDSINKEY IKKMKKKNY
KKEHMNKNNKDNNNNNNNSNKDDHININMNDNHRNYNDINLGPNSTDDSPTVSSLGNE
                                                                                                                                                                                                                                                                                                                                                                                                             KKIPLŮNGTYKYIDEEPSLKNINMYÄLKNOKIGIVGKSGAGKSTILLSILGLINISOG
TYTUBCRDIPTYNRKGEBSITOLIAGSSFYFYNMNIRTFIDPPNNFYDDEIVHALKLN
GINLGKNDLYKYMHKODMKSNYKKIIQTSKYINOSNNTILLTNOCIRYLSLYRLYLN
RHKYKIILIDEIPIRINNSVHDELNSFLIGRAKSFNYIIRNHFPNNTVLIISHHANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MALIP3.04, conserved hypothetical membrane protein, /note="MALIP3.04, conserved hypothetical membrane protein, len: 203 aa, similarity: P. falciparum chromosome 2, PFB0110W, 096126 predicted integral membrane protein (255 aa), fasta scores: opt: 335, E(): 4.9e-15, (36.1% identity in 191 aa overlap)"
RALYEHYIHMHKLCTDYEKKLIQPNEILDKDLINNKNISSYNNKKSKLVNYNIPFNEN
YLQKCLMDDNNFYLYLLDDIFTSLDPSISKKIFSNLFCKEDNISFKDNCSFIISMNKS
                                                                                                                                                                                                                                                                                                                                                 LSTLGYCISFSARLGVIIKFLLCDYTHIEKEMCCVQRLEEFAKISNKENASMNKENEL
NVITTQTYKEKNENISDKISAIVEYKNVSLSSIINSSQDDESKKYGIKFENVYVSYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="region containing small subunit, 5.8S and large subunit rRNA genes and spacer regions"
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36854. .36863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/product="conserved hypothetical membrane protein,
MALIP3.04"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23896. .31533

/gene="rRNA"

complement(foin(31966. .32476,32675. .32775))

/gene="MALIP3.04"

/gene="MALIP3.04"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSCCDYIYVLRKGEITYRCSYEDVKTQSELSHLLEMDD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /
/gene="MAL1P3.05"
/note="MAL1P3.05"
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36744. 36749
/gene="MAL1P3.05"
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complement(join(38049.
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/gene="rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="garp
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DITTE STATEMENT OF THE SECOND 
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                                                                                                                                                                                                         /translation="mnvLFLSYNICILFFVVCTLNFSTKCFSNGLLKNQNILNKSFDS
ITGRLLNETELEKNKDDNSKSETLLKEEKDEKDDVPTTSNDNLKNAHNNNEISSSTDP
                                                                                                                                                                                                                                                                          THIINVNDKDNENSVDKKKDKKEKKHKKDKKEKKEKKDKKEKKDKKEKHKKEKKHKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aaaccaataagttttaagcaatatatttactcagctattttacaagatttttataaagaaa 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 taaattatgtgagagattcagtagaatctatattaaatcaaacgcttactgattttgagt 100
aa), fasta scores: 97.6%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="potential splice donor sequence, aag/gtaaca"
join(45401. 46396,46562. .50233)
/gene="MALIP3.07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cagttgtagataatagaataaaaatcttgcttaatgaagaaaatattggtttagcatcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gtttgaacaaagcggtgaaaatttctaagggagaatatatttttagaatggatgctgatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atatttcatatccaagtagatttgataagcaaattcgttttatggaggaaaattcattgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gagaaagtaataaaatatacttaactaatgatatacggaagatgttattgaatagatcta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acceptor sequence"
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                                                                                                    garp protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 88.6; DB 3;
Pred. No. 3.9e-05;
0; Mismatches 424;
to GARP_PLAFF (678
                                    identity in 678 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(39996. .40005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"potential splice a complement(40204. .40209)
                                                                                                                                 /protein_id="CAB63561.1"
                                                                                                                                                                         /db_xref~"GI:6594249"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /qene="qarp
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les 395; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
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Consensus quality: 33034 bases at least 030
Consensus quality: 33034 bases at least 030
Consensus quality: 33871 bases at least 030
Estimated insert size: 4280; agarose-fp estimation
Estimated insert size: 36477; sum-of-contigs estimation
Quality coverage: 6.56 in 020 bases; agarose-fp estimation.
* NOTE: This is a "working draft' sequence. It currently
* consists of 6 contigs. The true order of the pleces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                     DNA linear HTG 03-JUL-2001
LLNLFOS-20C5, WORKING DRAFT
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Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Malnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 36977)
DOE Joint Genome Institute.
                                                                                                                                  9206 ATAATTAAATATATAAAATATAATAAATAAAATTAAAATTAAATTAAATTAAATTAAAT 9265
                                 aatcttatattgatatcacaaaaattactaattacttcaagagtatgtgataaagaaac
                                                                                                761 gctatactcagcaagagctctctaaatattttgagctaaaatctacccctagtattacta
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contig of 2068 bp in length
gap of unknown length
contig of 2222 bp in length
gap of unknown length
contig of 7465 bp in length
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contig of 9216 bp in length
gap of unknown length
contig of 13926 bp in length.
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Center clone name: LLNL-FOS_20C5
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Homo sapiens chromosome 19 clone
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                                                                                                                                                                                                                                                                                                                       SEQUENCE, 6 unordered pieces.
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36977: contig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           87 tactgattttgagttcataattgtcattgataatccaagtagaggtgatttaaagcaatt 146
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Pred. No. 0.0015;
0; Mismatches 475; Indels 20;
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                                                                                                                                   7254 9 10688
1. .36977
/organism="Homo sapiens"
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/chromosome="19"
                                                                                                         /clone-"LLNLFOS-20C5"
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Similarity 46.78;
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/translation="MNILLFGKTGQVGWELQRALAPLGNLIALDVHSTDYCGDFSNPEGVAETORSIRELion="MNILLFGKTGQVGWELQRALAPLGNLIALDVHSTDYCGDFSNPEGVAETVSIREDIIVAAAHTAVDKAESEPKRAQLINATSVEATAKAAREVGAWTHYSTDYVFPGTGEIPWLETDATAPLNVYGETKLAGEKALQEYCAKHLIFRTSWVXAGKGNNFVKTMLRLAKEREELAVINOPGAPTGAELLADCTAHAIRVDVAGLYHVAGGTTTWYDYAALVFEEARKAGIPLALNKLNAVPTAYTTPARRPHNSTLNTEKFQQNFALVLPPWQVGYKRMLNELFTTYVI"
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GRGYAMLDTGTHGGLIFBANFIATIEERQGLKVSCPEEIAYRKGFIDSEQVKVLAEPL
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PRITRGGGDLFLASYDDKIKSINVPVNIYTAGPIINYIYTFSPYSFNKMMEKDFNTT
EFTYGSRFFPFYNILSKLYGNERVVIIDENAYIPFRHNIFSVVKDYSDFGFWGVIL
IPFTIGLICGKSIKSFYLTARLSKIDYSYGILGVFFLSYILYSPLXNILSFGKFFIPL
VMMLFLSILFRVK
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FNFIGKWPEDYFWYSEPFPIIDENNKDVRYSFREPFLSHYIGNASVCTVWNTLERERR
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DDIWFKAMTLLSGRKCTRVNDFNILFPPVLGSQKQSLKKINVDSSENNNDKQLNMVFR
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                                                                                                                                                                                                                                                                                                                               /note="RmlA"
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1138. .2223

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                                                                                                                                                                                BCT 04-NOV-2001
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Wang, L., Qu, W. and Reeves, P.R.
Direct Submission
Submitted Submission
Submitted Sydney, Sydney, NSW 2006, Australia
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Wang, L., Qu, W. and Reeves, P.R.
Sequence Analysis of Four Shigella boydii O-Antigen Loci:
Implication for Escherichia coli and Shigella Relationships
Infect. Immun. 69 (11), 6923-6930 (2001)
                                                                                                                                                                              AF402315 10911 bp DNA linear BCT 04 Shigella boydii serotype 9 O-antigen gene cluster, partial
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Shigella boydii
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Y07786.1 GI:2244680
galactosyltransferase: mannose-1-phosphate guanylyl transferase;
ORF21x9 gene; ORF34x7 gene; ORF35x9 gene; ORF39x2 gene; ORF40x0
gene; ORF40x1 gene; ORF41x3 gene; ORF41x8 gene; ORF41x9 gene;
ORF50x8 gene; ORF54x5 gene; ORF56x5 gene; oxido-reductase; Rfc-11ke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
1 (bases 1 to 16265)
Manning,P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Revised by submittor 20-ocT-1996
2 (bases 1 to 16265)
Strocher, U.H., Parasivam,G., Dredge,B.K. and Manning,P.A.
Novel Vibrio cholerae 0139 genes involved in lipopolysaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Manning, University of Adelaide, De
3y, GPO Box 498, Adelaide S A 5005,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9202 AAAGATGCATTTGATGATATAA---AAATGCCATTAATTAGGACTGGTCAAGATTATGCG 9258
                                                                                                                                                                                                                                                                            attcgtttttatggaggaaaattca---ttggatttctcagcaactctaatagaattgata 369
                          gatttaaagcaattettaacagaatatteagttgtagataaaaaaaaatettgett 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cagtatagattaaacgagaatggaatatcacaaaccaataagtttaagcaatatttac
                                                             8842 TCAACACCGAAAATTATAAAGAAATTTGCTGCTCAAGATCCTCGGATAAATTGTATTCT
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                                                                                                                                                                                                                                gaccaaaaaggaaatttagtatataaacaacgagaaaagtaataaaaatatacttaactaat
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V.cholerae ORF's involved in lipopolysaccharide synthese.
Y07786 Y07787
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SISTILVGLEJLASIVUDNYIIIYHLLARFVFLKASFFESQARFVIYERINFFGNNK
NITVYFFCSRAVCLGIIGLIFRIKILSF VIETFYGKRETAAHLNLDILAIAFPAFLN
GIMSVSGFLFRGNIKYLNVTIIIAGCVSIPVCYFLSSSYPQISTSIAYVVAEGLISLI
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Pred. No.
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8163. .8696
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                                                                                                    /note="Wzx"
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Best Local 8
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BCT 30-NOV-1997

Dept

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                                                                                                                                            SVVFIQFKQTAMAMIYGLAFSQIFFSVILYNIITSEQEFSIVKIKSAFNKHYMKGVLE
FTLPVTITLLLQWGQTASFRLIVEDLYSAQILAFIAVGMTLSGAIFSALESLSTQFYM
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PVILALSYLTTLSIMPYNMKKLLSIRFEFLNPAIASLTLPLLVMHLLSITPTLFNSF
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                                                                                                  FYMFRYEQYFSIAEYSVFIVVSVIALIHGVLLNATNVLVSRVKFTVYAVLTLFIGLIL
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EGGGVDEKGIVTALECDKAPALKVGDVVQTDPRYFRPAEVETLGDPSKAKQKLGWT

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TKLKARGWSHGTSLEAGIEKTYQFYLNEYYQAVASVIGYTGRFKHDLSKPVGMRQKLIDD
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KMYAYWIVVNYRESYGMYACNGILFNHESPRRGETFVTRKITRGLANIAQGLEKCLYM
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adiwpelertorgamgriqildarakkosvivetiekpdpqtlisdimavgryuls
adiwpelertorgamgriqildarak"
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                                                              Submitted (18-DEC-2001) Microbiology, The University of Sydney, Sydney, NSW 2006, Australia Location/Qualifiers
      Huskic, S., Cisterne, A., Rothemund, D. and Reeves, P.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="wbgM"
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      Wang, L., Huskic, S.
Direct Submission
Submitted (18-DEC-
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                                TITLE
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                                                                                                                                FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8934 AGCAAACATTTCTGATTTTGAATTTATTATTATCATTAATGACGGTTCGAC-----TGATA 8987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8877 TTATGTCTGTTTATAATG---GTGAAAATATCTTGGAGAAGCCATAGATAGTATTCTTA 8933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8988 AGACACTAGAGATAATAAAGTCATATATGAAGAAGGATGACCGTATTGTATTGGTTTCAA 9047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9048 GAGAAAACAAAGGGCTAATAGTAAGCCTAAATGAAGGGCTAGATTTAGCTAAAGGGCAAT 9107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     taaagcaattottaacagaatattcagttgtagataatagaataaaaatottgcttaatg 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atatttttagaatggatgctgatgatatttcatatccaagtagatttgataagcaaattc 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atcaaacgcttactgattttgagttcataattgtcattgataatccaagtagaggtgatt 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ttatgtcggtatataatgagcctttaaattatgtgagagattcagtagaatctatattaa 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Mang,L., Huskic,S., Cisterne,A., Rothemund,D. and Reeves,E
The O-antigen gene cluster of Escherichia coll 055:H7 and
identification of a new UDP-GICNAc epimerase gene
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al Similarity 57.2%;
183; Conservative
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Matches
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 77.2; DB 1; Length 27730;
Pred. No. 0.0026;
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237; Conserv
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8417. 9289
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GPLDFTLGFGWGYLGNRANLSGDKISSTDCGRDSNYGGNGGMLDLGRMFTGCTALFGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (pases 1 to 46721)
Yamasaki,S., Shimizu,T. and Hoshino,K.
Direct Submission
Submitted (14-APR-1998) Shinji Yamasaki, Internatinal Medical
Center of Japan, Research Institute: Toyama 1-21-1, Shinjuku, Tokyo
162-8655, Japan (E-mail:shinji@rl.imcj.go.jp, Tel:+81-3-3202-7181,
Fax:+81-3-3202-7364)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNNSNPQTSDYKSFIHIPDENKLFFFSLNHFNQLSFEPTNKLGRDVSVNSRRGRPLLL
TAYBRTNQDVIQNLESFKFRATNALGSLGGEIDLD IIDQRDTPWTVPSDVELSSAQLE
VDGROFNAPYAYLWQSLNTSSEDKYSYSNLINYDNYYLKLKCKEISPPSEPYWKFQHV
SRGTSSITSHLSAENILDGFNPEPPTLGICONNYQLITTHTQYTDNTILKLLID
SELTVPSGLPFFIKOTTYSPYHNELPVWKFDSPILDQELKEIKDFSVSWIKTPESSIT
ETFLYQYQDLYKRTLGSELIDPSIDNIPLLKNISAQQDQDLLKRQPYWWLLEE"
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YCLDREIPFLYASSAATYGETDTFIEBPQYEGALNVYGYSKQQFDNYVRRLMLDAKQH
DETLSOITGFRYFNYGPREOHKGSMASVAFHLNNONNAGENPKLFAGSENFKRDFVY
VGDVAAVNLWFLDHGVSGIFNCGTGKAESFNEVAKAVIAFHGRGEVETIPFPDHLKGA
YQEFTEADLTKLRAAGCDVQFKSVAEGVAEYWALINRK"
COMPLEMENT (8924. . 10441)
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/db_xref="GI:374296"
/translation="MIIVTGGAGMIGSNIIKALNERGITDILVVDHLKNGRKFKNLVD
                                                                                                                                                                             AB012956 46721 bp DNA linear BCT 16-OCT-1999 Vibrio cholerae genes for O-antigen synthesis, strain MO45,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MHKPTISSVIALTLGCGGGESGNSGNTTPPVKYFNVSFLDLDN
IAINTQTNCQIFGYNEDQTKKIVAYRSAPENNYQIVVHDEHGNFVRRYSNSTETNGLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamasaki,S., Shimizu,T., Hoshino,K., Ho,S.T., Shimada,T., Nair,G.B. and Takeda,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The genes responsible for O-antigen synthesis of vibrio cholerae 0139 are closely related to those of vibrio cholerae 022 Gene 237 (2), 321-332 (1999) 99453293
Db 12172 TCAAAATTTACCGGAATATTTATTCTATTACAGGTTGCATGA 12213
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/gene="gmhD"
/note="probable LPS core synthesis"
/codon_start=1
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/organism="Vibrio cholerae"
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complement(8924..10441)
/gene="wbfA"
/note="unknown"
/codon_start=1
/transl_teable=11
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complement(10522. .12714)
/gene="wbfB"
/note="unknown"
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complement(7866. .8810)
/gene="gmhD"
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Location/Qualiflers
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FPGSSYSTQEKSHGRLETRVALVNRDLSVLGDIEHEWPGLKSMGIVASIRQESAVATE
QDVSIRYICSKELEAQTLLEATRSHWGVEVMHWSLDTAFCEDNSRIRADDRAEAFAR
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20961. .22079
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LFVPTFRNTISIMGEVQVPVTYLLAFVEBASRSKALGRWYVOLSRIMRDEGADFMLEDGGSV
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11492
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18485. 119492
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//db_xref="G1:3724305"
//db_xref="G1:372430
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DINKVMKERDVAEAHRSTAFLNEQIALTNVADIRTVLYKLIEEQAKTIMFAEVRDEYV
FKTIDPALAPEEKAKPKRALICVLGTLLGGMLGVAIVLVRFAFRKAGKNHEHADVRET
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'note="probable transport of capsular precursors"
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Pred. No. 0.0023;
0; Mismatches 128; Indels
                                                                                                                                                  /protein_id="BAA33592.1"
/db_xref="G1:3724303"
                                                                                                    /transl_table=11
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/gene="IS1358"
19650. .20777
/gene="IS1358"
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/note
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AC106820 177509 bp DNA linear HTG 12-JAN-2002
Homo sapiens chromosome 16 clone RP11-715J22, WORKING DRAFT
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Unpublished
2 (bases 1 to 177509)
DoE Joint Genome Institute.
Direct Submission
Submitted (12-JAN-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Greek, CA 94598, USA
Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Consensus quality: 173535 bases at least Q40
Consensus quality: 175401 bases at least Q30
Consensus quality: 17541 bases at least Q30
Consensus quality: 175541 bases at least Q30
Estimated insert size: 176009; agarose-fp estimation
Estimated insert size: 177009; sum-of-contigs estimation
Quality coverage: 11.95 in Q20 bases; agarose-fp estimation

* NOTE: This is a 'working draft' sequence. It currently

* consists of 6 contigs. The true order of the pieces

* is not known and their order in this sequence record is
29762 AGACACTAGAGATAATAAAGTCATATGAAGAAGGATGACGTATTGTATTGTATTGAA 29821
                                                                                                                                                                                                                                            29822 GAGAAAACAAAGGGCTAATAGTAAGCCTAAATGAAGGGCTAGATTTAGCTAAAGGGCAAT 29881
                                                                                                                                                                                                                316
                                                                                             aagaaaatattggtttagcatcaagtttgaacaaagcggtgaaaatttctaagggagaat
                                                                                                                                                                                                             257 atatttttagaatggatgctgatgatatttcatatccaagtagatttgataagcaaattc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig of 1009 bp in length
contig of 10741 bp in length
contig of 10741 bp in length
gap of unknown length
contig of 18696 bp in length
contig of 13058 bp in length
gap of unknown length
gap of unknown length
contig of 55616 bp in length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
contig of 77889 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center Project Name: 1569302
Center clone name: RPCI-11_715J22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalla; Eutharia; Primates;
1 (bases 1 to 177509)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE, 6 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                     29942 AGTTTTTAGATAGTAATCCA 29961
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AC106820.1 GI:18139370
                                                                                                                                                                                                                                                                                                                                      317 gttttatggaggaaaattca 336
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43904:
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="chamically treated genomic DNA (Homo saptens)-organism="synthetic construct"
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1.249.980-seq 03 600.001 949.980-seq 04 900.001
1.849.980-seq 05 1.200.001 2.149.980-seq 06 1.500.001
2.449.980-seq 07 1.800.001 2.149.980-seq 08 2.100.001
3.049.980-seq 11 3.000.001 2.749.980-seq 10 2.700.001
3.649.980-seq 11 3.000.001 3.673.78 <223>-original length of seq 2: 3.673778 <223-split as follows.-seq 18 1.200.001
1.549.980-seq 19 1.500.001 1.849.980-seq 20 1.800.001
2.149.980-seq 21 2.100.001 2.449.980-seq 22 2.400.001
2.749.980-seq 22 3.700.001 3.649.980-seq 26 3.600.001
3.573.778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 atgaagaaaatattggtttagcatcaagtttgaacaaagcggtgaaaaatttctaagggag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              374 aaaaaaggaaatttagtatataaacaacgagaaagtaataaaaatatacttaactaatgata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 349980;
                                                                                                                                                                                                                                                                        Diagnosis of known genetic parameters within the mhc Patent: WO 0200932-A 6 03-JAN-2002; Epigenomics AG (E) Location/Qualifiers
                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.1%; Score 76.2; DB 6;
44.6%; Pred. No. 0.002;
iive 0; Mismatches 423;
 68007 AATATATCTAATTATGGATATTATATATATAAT 67973
                                                                                              DNA
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Olek,A., Piepenbrock,C. and Berlin,K.
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                                                                                          AX344555 34980 bp
Sequence 6 from Patent W00200932
AX344555 AX344555.1 GI:18492441
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synthetic construct
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Matches 341; Conservative
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AX344555/c
                                                                                                         DEFINITION
                                                                                                                                                                                                  ORGANISM
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                                                                                                                                                                                                                                                                        TITLE
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KEYWORDS
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                                                                                                                          others
                                                                                                                                                                                                Score 77; DB 2; Length 177
Pred. No. 0.0018;
0; Mismatches 460; Indels
                                                                     /chromosome="16"
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/45006 c 43244 g 43065 t 500 oth
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                1. .177509
/organism="Homo sapiens"
/db_xref="taxon:9606"
cocation/Qualifiers
                                                                                                                                                                                                tch 8.2%;
al Similarity 45.6%;
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554 caataagaggagctctggctgatttcaaaatcggcttactcaataaagtacttttacagt 613
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GenCore version 4.5 dht (c) 1993 - 2000 Compugen	<pre>iarch, using sw model : 2, 2002, 10:39:54 ; Search tim (without 7780.586</pre>	-09-900-038A-2 9 atgaattatagtatcattatga	TY_NUC 10.0 , Gapext 1.0	.07 seqs, 6748477542 residues	<pre>sat1sfying chosen parameters: : 0 :: 2000000000</pre>	m Match 0% im Match 100% ig first 45 summaries	em_estba:* em_esthum:* em_esthum:* em_estrin:* em_estro:* em_estro:* em_estro:* em_estro:* em_estro:* gb_estl:* gb_estl:* gb_gss:* em_gss_lnw:* em_gss_lnw:* em_gss_lnv:* em_gss_lnv:* em_gss_lnv:*	umber of results predicted or equal to the score of nnalysis of the total scor	SUMMARIES	Length DB ID	101 101 101 101 101 101 101 101 101 101
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	62	62.2		867	7	CNS075BG	
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c 23	61	61.8		756	12	BH575203	BH575203 BOGYW19TR
24	61	9		777	Н	CNS025WB	AL182612 Tetraodon
25	61	9:		916	-	B09084	ഹ
26	61	61.6		945	_	CNS04D0K	AL285149 Tetraodon
27	61	61.6		994	-	CNS04NOJ	
28	61	61.4	6.5	1085	12	CNS016YR	
	61	7		938	12	CNS006TJ	9
c 30	61	7		1101	12	CNS0175J	
31	9	8.		1101	12	CNS008X3	
32	9	8.		1101	12	CNSOOYWL	AL096927 Drosophil
c 33	9	8.		1101	12	CNS05AB2	
34	9	8.		1200	12	CNS016CO	
35	9	9.		1190	12	CNS020N7	
36	9	60.4	6.4	734	15	CNS010MP	AL099163 Drosophil
37	9	60.4	6.4	849	σ	AL578920	AL578920 AL578920
c 38	9	60.4	6.4	1101	15	CNS014XJ	
39	9	60.2	6.4	886	13	BH177277	
40	09	.2	6.4	886	12	CNS07JUX	
41	9	.2	6.4	966	12	CNS00FUH	
42	9	60.2	6.4	1101	12	CNS003BD	
43	9	. 2		1101	12	CNS00EO7	
C 44	9	.2	9.4	1190	15	CNS020N7	~ ~
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		BACR	29B23	BACR29B23 of RPCI-98	- 98	library from Dros	library from Drosophila melanogaster (fruit
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db.xref="taxon:7227"
/clone_libb="RPCI-98"
/clone=BACR08K10"
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Web: www.genoscope.cns.fr.

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                                                                                              Drosophila melanogaster genome survey sequence T7 end of BAC: BACKSBR33 of RPCI-98 library from Drosophila melanogaster (fruit AL069706
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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/db_xref="texon:7227"
/clone_lib="RPCI-98"
/clone="BACR29B23"
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llarity 33.7%; Pred. No. 0.0021;
Conservative 105; Mismatches 310;
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Direct Submission
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Email: jecker@atgenome.bio.upenn.edu
Seq primer: Sp6
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High quality sequence stop: 138.
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/clone_lib="IGF"
/sex="hermaphrodite"
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Other_GSSs: F19M10-T7
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/clone="BACN10102" /note="end : SP6"

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Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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/plasmid="pheloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
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Drosophila melanogaster genome survey sequence T7 end of BAC
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  159 others
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                                                                                                                                  84; Mismatches 426;
                                                                                        12;
                                                                                        69.6; DB No. 0.034;
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  308
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                                                                                        7.4%;
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21
                                                                                                             Similarity
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GSS 04-JUN-1999

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collaboration with the Berkeley Diosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BAGs. For further information please see http://www.fruitily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pater de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (02-UUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRx cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of
                                                                                                               Drosophila melanogaster genome survey sequence T7 end of BAC # ARCR27A24 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence. AL071865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cccacccaacgtggtgcgtaaaaaagaaagttttcgataagttaatgggatatagagatt 526
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Pterrygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilldae; Drosophila.
I (bases 1 to 928)
                                                                                          p DNA linear GSS 04-JU survey sequence T7 end of BAC
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Pred. No. 0.053;
; Mismatches 217;
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/clone_lib="RPCI-98"
/clone="BACR27A24"
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31.3%; Pred
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                                                                                                                                                                                                                                           Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-ond sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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/organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lb="DrosBAC"
/clone="BACN03B09"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC ilbrary was prepared by Kazutoyo Oscogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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/db.xref="taxon:7227"
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11 Similarity 18.7%; Pred. No. 0.052;
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Drosophila melanogaster genome survey sequence T7 end of BAC BACN37F11 of DrosBAC library from Drosophila melanogaster (fruit AL108152
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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/plasmid="pBeloBAC11"
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                                                                                                                                                                                                                                                                                                            gatatttcatatccaagtagatttgataagcaaattcgttttatggaggaaaattcattg 339
                                                                                                                                                                                                                                                                                                                           ataaacaacgagaaagtaataaaatatacttaactaatgatatacggaagatgttattga 451
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                                                                                                           ttaaattatgtgagagattcagtagaatctatattaaatcaaacgcttactgattttgag 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           724 GGGAAAMCGKKKAMAGDAAKKGAAAAAAAAAAHDADAAAAAAAAAAAGGWAAAAKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    664 KKMAGRAKAKACAAAKKAAGKTCAGACACKAKAAAAAAGDCKKMGGKDAKAAARAKMKAA
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                                                                                                                                                                                                                                                                                  RKBGKACAGAAAAAAKCGSAAMMBTAGKKGKAGGCDKCCMAADTWDKTWATTYKCAAAK
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                                                                                  10;
                                                          Length 1101;
                                                        Query Match 7.3%; Score 68.2; DB 12; Length Best Local Similarity 31.1%; Pred. No. 0.056; Matches 276; Conservative 160; Mismatches 441; Indels
           others
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Submitted (23-JUJ-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       622
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Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATMNKAWHWHTABTAKATAWAAWADTAKAAWDGWAAWAATDKWDTWKWKADADTTATAK
TATMNKAWHWHTABTAKATAWAAWADTAKAAWDGWAAWAATDKWDTWKWKADADTTATAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aaatcttgcttaatgaagaaaatattggtttagcatcaagtttgaacaaagcggtgaaaa
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Drosophila melanogaster genome survey sequence SP6 end of BACN11B06 of DrosBAC library from Drosophila melanogaster fly), genomic survey sequence.
AL103554
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Pred. No. 0.082;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Drosophila mm/plasmid="pBeloBAC11"
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/clone_lib="DrosBAC"
/clone="BACN11B06"
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Drosophila melanogaster
                                                                                                          AL103554.1 GI:5615165
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GSS 26-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster genome survey sequence T7 end of BAC BAC BACILILI of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

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GENOME STATE OF SECTION OF SEQUENCE.
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                                                                                                                                                                 41 taaattatgtgagagattcagtagaatctatattaaatcaaacgcttactgattttgagt 100
751. WITAAAIAAAAAAAAITITAITITIATITWITAITWAAAWITITWITITWAAITWWYITIA 692
                                                                                                                                        815 ttactattagaaaactatatatttgtttatattttatactttaagtctcccttggttagga 874
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                                               agaaacgctatactcagcaagagctctctaaatattttgagctaaaatctaccctagta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1025)
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                                                                                                                                                                                                                                                                  S71 ATWWWATAAAAAAATWWWTTATTATAAWAAATTATTAWAWTTG 527
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1. .1025
/organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="bACN11111"
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31.6%; Pred. No. 0.095;
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- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be filters for hybridization from the BACPAC Resource Center can be
                                                         Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACKS2901 of RPCI-98 library from Drosophila melanogaster (fruit AL069440
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
(bases 1 to 1101)
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Location/Qualifiers
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/db_xref="taxon:7227"
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This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exvazzii, Zygosaccharomyces rouxii, Saccharomyces servazzii, Zygosaccharomyces rouxii, Jactis var. lactis, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
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Souchet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M. Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuveqlise,C., Ozier Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Welssenbach,J.
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FEBS Lett. 487 (1), 3-12 (2000)
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                                           atatttcatatccaagtagatttgataagcaaattcgttttatggaggaaaattcattgg 340
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424 TTATRTAKKTTAAAAAAAAGTGTKWTRATKKKTGKTGDKAARAAADAAATTAAAAAAA 365
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                                                                                                                                                               521 gagatttagtacctgttgaagattatgattttgcaataagaggagctctggctgatttca 580
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                                                                                                                                                                                                                                                                                          461 tacttgcccacccaacgtggtgcgtaaaaaaaaagaaagttttcgataagttaatgggatata
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FEBS Lett. 487 (1), 47-51 (2000)
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Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 t 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

Location/Qualifiers
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                                                                                                                             /organism="Saccharomyces servazzii"
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                                                                                                                                                                                                                                                                     91
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Wing,R.A., Frisch,D., Yu,Y., Main,D., Ramb,
.D., Wood,T.C., Leslie,A. and Wilkins,T.A.
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11.6%; Pred. No. 0.12,
.ve 27; Mismatches
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   of the genetics, development, and evolution
                                                                                                                                                                                                                                                                                      /cullivar="8400"
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/clone=ilb="GGSSypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
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                                           Contact: Wing RA Clemson University Genomics Institute Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288
Email: rwing@clemson.edu Total High Quality bases = 126 Seq primer: TAATACGACTCACTATAGGS High quality sequence start: 3 High quality sequence start: 3 High quality sequence start: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        389;
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/organism="Gossypium arboreum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 65.4; DB Pred. No. 0.16; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pbK-CMV;
57 c 18 g 36
                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                        /lab_host-"E. coli"
An integrated analysis
of the cotton fiber
Unpublished (2000)
                                                                                                                                                                                                                                                                             /strain="AKA
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nilarity 46.1%;
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Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                  CNSO20K7 1092 bp DNA linear GSS 12-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 222L11 of library G from Tetraodon nigroviridis, genomic survey
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Ross: 1 to 1092)

Ross: Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Meissenbach, J., Billault, A., Quetler, F., Saurin, W., Bernot, A. and Characterization and repeat analysis of the compact genome of the Unpublished
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence ID : COAG222CF06LP1-end : T7" g 262 t 113 others
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ilarity 36.5%; Pred. No. 0.16;
Conservative 59; Mismatches 207;
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GSS; genome survey sequence.
Tetraodon nigroviridis.
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                             August 2, 2002, 12:22:04; Search time 210.05 Seconds
   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                       Total number of hits satisfying chosen parameters:
                                                                               1736436 seqs, 858457221 residues
                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    nucleic search, using sw model

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Maximum DB seq length: 200000000
                                               US-09-900-038A-2
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                                               Title:
Perfect score:
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DNA encoding enzym Nucleotide sequenc Plasmodium var-7 p 90 kb subunit of S Human immune syste Human immune syste Human immune syste Plasmodium var-7 p

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Human immune syste

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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æ	Query Match	7.5	7.3	7.3	7.3	7.1	6.9	6.9	6.8	6.8
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	ABL34155 standard; DNA; 15548 BP.
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AC AX	ABL34155;
	26-MAR-2002 (first entry)
	Human immune system associated gene SEQ ID NO: 2128.
	Human; immune system disease; cytosine methylation; antiasthmatic;
	antiarteriosclerotic; antianaemic; cytostatic; nootropic;
	neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
	untirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW a	antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW a	acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
	neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
	gene; ds.
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	Homo sapiens.
XX	
	WO200200928-A2.
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	02-JUL-2001; 2001WO-EP07537.
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347 cagcaactctaatagaattgatagaccaaaaaggaaatttagtatataaacaacgagaaa 406
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                                                                                                                                                                                                                                           The present invention provides a number of human immune system associated dense which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, Alzheimer's disease, Alzheimer's disease, and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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                                                                                                leic acid comprising fragment of chemically modified gene, useful diagnosis and treatment of diseases associated with abnormal
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                                                                                                                                                                                                Claim 1; SEQ ID NO 2128; 32pp + Sequence Listing; German
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Pred. No. 0.00037;
0; Mismatches 413;
Berlin K;
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ilarity 44.3%;
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  Piepenbrock C,
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune system disease; cytosine methylation; antiasthmatic;
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for diagnosis and treatment of diseases associated with abnormal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immune system associated gene SEQ ID NO: 2267.
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0; Mismatches 264;
                                            11420 TACTTAATTATTATAACAACGAAATATT 11392
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01-SEP-2000; 2000DE-1043826
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/note= "ORF8; e
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52.5%;
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           AAW88317" CDS
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                                          1624 TACATAAAACCCTCATAACAAAACAAATTATCAAATATAACAAATCCAACCTTA 1565
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                                                                                                                                                                                                                                                                                                                                                                                                            O antigen; O157 antigen; diagnosis; wbdN gene; wzx gene; wzy gene; wbdP gene; wbdO gene; wbdR gene; transferase; polymerase; flippase; diarrhoea; haemorrhagic colitis; ds.
                                                                                                                             gtaataaaatatacttaactaatgatatacggaagatgttattgaatagatctatacttg
                                                                       467 cccacccaacgtggtgcgtaaaaaaagaaagttttcgataagttaatgggatatagagatt
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/product= O_antigen_flippase
/note= "wzx gene (ORF4), this region is
specifically claimed in Claim 6; encodes
4132..5232
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/note= "wbdN gene (ORF1), this region is
specifically claimed in Claim 6; encodes
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/note- "per gene (ORF5); encodes AAW88316"
5257..6471
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"way gene (ORP2), this region is
specifically claimed in Claim 6;
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/note- "wbdP gene (ORF6), this region is
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/note= "wzy
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This is the nucleotide sequence of a gene cluster involved in the biosynthesis of the Escherichia coli 0157 O antigen. The gene cluster was obtained by PCR amplification of E. coli 0157.87 strain (C664-1992) MAN using primers (see AAX06752-63) based on 0 antigen gene sequences. 12 Open reading frames within the gene cluster were identified on the basis of homology to known sequences. The genes encode proteins (see AAW88312-33) involved the synthesis of sugars present in the polysaccharide antigen, and in the transport or processing of polysaccharide or oligosaccharide units. The use of nucleic acid molecules derived from particular P-PSDB; AAW88312, AAW88313, AAW88314, AAW88315, AAW88316, AAW88317, AAW88318, AAW88319, AAW88320, AAW88321, AAW88322, AAW88323. assembly and transport genes, particularly wbd (transferase), wax (flippase) and wzy (polymerase) genes, within O antigen gene clusters improves the specificity of methods for the detection and identification of O antigens, e.g. in tests of food or faecalderived samples, or samples from patients. The O antigen is a major virulence factor of enteropathogenic E. coli strains that may play a role in gene cluster /note= "wbdR gene (ORF12), this region is specifically claimed in Claim 6; encodes AAW88323" Length 14024; Nucleic acid molecules specific for bacterial polysaccharide antigens - useful for detecting specific strains in, e.g. food, faeces or patient samples noite "manc gene (ORF10); encodes AAWBB321" [0523.,11893 /note= "manD gene (ORF11); encodes AAW88322" 12007..13123 Seguence 14024 BP; 4546 A; 2263 C; 2832 G; 4383 T; 0 other; specifically claimed in Claim 6491..7609 Score 68.2; DB 20; Pred. No. 0.00084; g "ORF7; encodes AAW88318" /note= "ORF9; encodes AAW88320" 9071..10519 encodes AAW88319" /product- N-acetyl_transferase cause diarrhoea and haemorrhagic colitis.

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97US-0066009.
97US-0044031.
97US-0046655.
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16-MAY-1997;
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    Gaps
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9
    Indels
  173;
    Mismatches
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serotype in the sample. (I) are useful for: (1) detecting the presence of E. coli of H serotype in a sample by hybridising at least one or a pair of (I) to any E. coli in the sample and detecting the hybridised nucleic acid molecules; and (2) for detecting the presence of both o and H serotypes of E. coli by hybridising at least one or a pair of (I) to any E. coli present in the sample and detecting the hybridised nucleic acid molecules. (I) is particularly useful for detecting the combination of O and H antigen. Hybridised (I) when using at least one (I) is detected by southern blot analysis and, when using a pair of (I), is detected by polymerase chain reaction (PCR). AAZ56399 to AAZ56420 represent primers used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 14024;
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                                                                                                                                                                                                                                                              982 nucleotide sequences isolated from the Enterococcus faccalis genome.

AAX12038 to AAX13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faccalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faccalis in samples. They can also be used for progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faccalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faccalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              computer readable medium has been developed which has recorded on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4045 AAAAAGATTCAAGAATCTTTTTACTGAAAAATGAACAGAACATGGCCATTGCAAAGACCA 3986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                             New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.1%; Score 67; DB 20; Length 4915; 54.3%; Pred. No. 0.0014;
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                                                                                                                                                                                                        Claim 1; Page 759-761; 2084pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunity; immunogen; ganglioside; ds.
                                       Kunsch CA;
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(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Campylobacter jejuni OH4384.
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Matches 133; Conservative
                                     Dillon PJ,
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A reaction mixture for the synthesis of a sialylated oligosaccharide is useful for synthesising sialylated oligosaccharide such as ganglioside. I yegoanglioside or their mindrs. Glycosyltransferases are useful for chemo-enzymatic synthesis of oligosaccharides, including gangliosides and other oligosaccharides that have biological activity. The enzymes and nucleic acids that encode them are useful for studies of the pathogenesis mechanisms of organisms that synthesize ganglioside minates, such as C. jejuni and the nucleic acids are used as probes to study expression of genes involved in ganglioside minatic synthesis. Antibodies raised against the glycosyltransferases are also useful for analyzing the expression patterns of these genes involved in pathogenesis. The oligonucleotides for inhibiting expression of the Campylobacter oligonucleotides for inhibiting expression of the Campylobacter can mask the pathogens from the host's immune system. The
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Pred. No. 0.0032;
0; Mismatches 157; Indels 3
                                                                                                                 /product= Beta-1,4-galactosyltransferase
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Location/Qualifiers
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31-JAN-2000; 2000US-0495406.
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Best Local Similarity
Matches 172; Conserv
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181 aaaatcttgcttaatgaagaaaatattggtttagcatcaagtttgaacaaagcggtgaaa 240
                                    241 atttctaagggagaatatattttagaatggatgctgatgatatttcatatccaagtaga 300
                                                                                                                                                                                                      Blosynthetic locus; biosynthesis; lipid A biosynthesis; acetyltransferase; Beta-1,4-GallMc transferase; Beta-1,3-galactosyltransferase; alpha-2,3-sialyltransferase; sialic acid synthase; CMP-sialic acid synthetase; mimic; antibody; immunogen; ganglioside; ds.
                                             178 aaaataatccacaatgaaaaaaacttaggtcttttaagagcaagatatgaaggtgtgaaa
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note= "Open reading frame 6a"
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/note= "Open reading frame 10a"
complement (10554..11366)
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AAY97206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel glycosyltransferase polypeptides and polynucleotides useful biosynthesis of ganglioside and ganglioside mimics, as diagnostic reagents and as immunogen for producing antibodies
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Pred. No. 0.0034;
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51.8%;
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Matches 172; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system discorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid treukaemia, Alzheimer's disease, AlDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
acaaagcggtgaaaatttctaagggagaatatatttttagaatggatgctgatgatattt 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                           antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirhemmatic; antiarthritic; antidiabetic; antipsoriatic; antianifammatory; cancer; eye disease; arteriosclerosis; anaeute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                  Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tagataatagaataaaaatcttgcttaatgaagaaaatattggtttagcatcaagtttga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal cytosine methylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 375; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 986; 32pp + Sequence Listing; German
                                                                                                                                                                                          Human immune system associated gene SEQ ID NO: 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 64; DB 24;
Pred. No. 0.0048;
                                                         5662 TGTGAAGAGTGTATAAAATTTTAGATGAACA 5631
                                  tttgataagcaaattcgttttatggaggaaaa 332
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                                                                                                                   ABL33013 standard; DNA; 7597
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01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                               02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                   (first entry)
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Best Local Similarity 45.2
Matches 313; Conservative
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                                                                                                                                                                 26-MAR-2002
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                                                                                                                                           ABL33013;
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catatccaagtagatttgataagcaaat-tcgttttatggaggaaaattcattggatttc 345
                                                                                                                                                                          627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biosynthetic locus; blosynthesis; lipid A biosynthesis; acetyltransferase; glycosyltransferase; Beta-1,4-GalNAc transferase; Beta-1,3-galactosyltransferase; alpha-2,3-sialyltransferase; sialic acid synthetase; mimic; antibody;
                                                                                                                                                                      586 AAATAAATAAATAAATAAATAAATAAATAAACACATAAATAAATAAATAAATAAATAAAT
                                                                                                                                                                                                                                       agtaataaaaatatacttaactaatgatatacggaagatgttattgaatagatctatactt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              326 AAATAAATAAATAAATAAATAAATAATAAATAAATACATAAATAAATAAATAAA---TAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            actcagcaagagctctctaaatattttgagctaaaatctaccctagtattactattaga
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                                                                                                                                                                                                                                                                                               626 ACGTAAATAAATAAATAAATACATAAATAAATAAATACATAAATAAATAAATAAATAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           826 aaactatattttgtttatattttatactttaa 857
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1..1170
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us-09-900-038a-2.rng

(first entry)

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LPS core biosynthesis locus
            22-DEC-2000
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ij
                                                                                                                                                                                                          Statistical for synthesising simplifies of oligosaccharides such as ganglioside, lysoganglioside or their mimics. Glycosyltransferases are useful for chamo-enzymatic synthesis of oligosaccharides, concluding gangliosides and other oligosaccharides that have biological activity. The enzymes and nucleic acids that encode them are useful for studies of the pathogenesis mechanisms of organisms chart synthesize ganglioside mimics, such as C. jejuni and the nucleic acids are used as probes to study expression of genes involved in ganglioside mimics, such as C. jejuni and the cupyled in ganglioside mimics, such as C. jejuni and the nucleic acids are used as probes to study expression of genes involved in ganglioside mimics. Antibodies raised against the glycosyltransferases are also useful for analyzing the expression patterns of these genes involved in pathogenesis. The nucleic acids are also useful for designing antisense oligonucleotides for inhibiting expression of the Campylobacter coligonucleotides for inhibiting expression of the Campylobacter coligonaccharides are useful as diagnosing reagents or as therapeutics that can mask the pathogens from the host's immune system. The oligosaccharides are useful as diagnosing reagents or as therapeutics and as immunogens for producing antibodies. Bacterial glycosyltransferase can be used to catalyse the formation of cligosaccharides that are identical to the corresponding mammalian glycosyltransferase. The mammalian glycosyltransferase. The mammalian plycosyltransferase.                                                                                                                for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 cataattgtcattgataatccaagtagaggtgatttaaagcaattcttaacagaatattc 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aaattatgtgagagattcagtagaatctatattaaatcaaacgcttactgattttgagtt 101
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                                                                                                                                                                                                 reaction mixture for the synthesis of a sialylated oligosaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        quantities of the enzymes using relatively inexpensive prokaryotic expression systems.
                                                                                                            Novel glycosyltransferase polypeptides and polynucleotides useful biosynthesis of ganglioside and ganglioside mimics, as diagnostic reagents and as immunogen for producing antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 agttgtagataatagaataaaaatcttgcttaatgaagaaaatattggtttagcatcaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 63.8; DB 21;
Pred. No. 0.0049;
0; Mismatches 102;
                                                                                                                                                                    Disclosure; Page 99; 120pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA53720 standard; DNA; 11474 BP.
          (CANA ) NAT RES COUNCIL CANADA.
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Matches 138; Conservative
                                        Wakarchuk WW;
                                                                  WPI; 2000-524418/47.
P-PSDB; AAY97202.
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                                       Gilbert M,
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Best Local S
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Novel glycosyltransferase polypeptides and polynucleotides useful for
Biosynthetic locus; biosynthesis; lipid A biosynthesis; acetyltransferase; alycosyltransferase; Beta-1,4-GalNAc transferase; Beta-1,3-galactosyltransferase; alpha-2,3-sialyltransferase; siallac acid synthese; CMP-sialic acid synthetase; mimic; antibody; immunogen; ganglioside; ds.
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P-PSDB; AAY97200, AAY97201, AAY97202, AAY97203, AAX97204, AAX97205,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= Beta 1,2- galactosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= Beta 1,4-GalNAc transferase
/note= "Open reading frame 5a"
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                                                                                                                                                                                                                                                                                                                                    transferase
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/product= Glycosyl transferase
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6048..6923
                                                                                                                                                                                                                                                                       "Open reading frame 2b"
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2786..3955
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                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                     Campylobacter jejuni OH4384.
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31-JAN-2000; 2000US-0495406
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6924..7964
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9076..9741
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                                                                                                A reaction mixture for the synthesis of a sialylated oligosaccharide
is useful for synthesising sialylated oligosaccharide such as
ganglioside, lysoganglioside or their mimics. Glycosyltransferases
are useful for chemo-enzymatic synthesis of oligosaccharides,
including gangliosides and other oligosaccharides that have
biological activity. The enzymes and nucleic acids that encode them
biological activity. The enzymes and nucleic acids that encode them
care useful for studies of the pathogenesis mechanisms of organisms
that synthesize ganglioside mimics, such as C. jejuni and the
nucleic acids are used as probes to study expression of genes
involved in ganglioside mimetic synthesis. Antibodies raised against
the glycosyltransferases are also useful for analyzing the
expression patterns of these genes involved in pathogenesis. The
nucleic acids are also useful for designing antisense
oligonucleotides for inhibiting expression of the Campylobacter
enzymes that are involved in the biosynthesis of ganglioside mimics
that can mask the pathogens from the host's immune system. The
oligosaccharides are useful as diagnosling reagents or as therapeutics
and as immunogens for producing antibodies. Bacterial
and as immunogens for producing antibodies. Bacterial
structures and are easier and less expensive to produce in large
curretters and are easier and less expensive to produce in large
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       quantity, compared to the mammalian giycosyltransferase. The bacterial origin of the enzymes facilitates expression of large quantities of the enzymes using relatively inexpensive prokaryotic
ganglioside and ganglioside mimics, as diagnostic immunogen for producing antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterococcus faecalis; contig; detection; Enterococcal infection;
vaccine; attenuation; computer readable medium; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 11474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11474 BP; 4506 A; 1495 C; 1613 G; 3860 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 63.8; DB 21; Length
Pred. No. 0.0052;
0; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterococcus faecalis genome contig SEQ ID NO:201.
                                                                Claim 1; Page 86-90; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX13138/c
ID AAX13138 standard; DNA; 5154 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.8%; 56.8%; 1
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Matches 138; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression systems.
blosynthesis of
reagents and as
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Enterococcus faecalis

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982 nucleotide sequences isolated from the Enterococcus faecalis genome. AAX12938 to AAX13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1397 TCGCGAAGAAAACGGACATATTTCAGAAGCAACTAACTCAGCTTTGTCGATTGCTACTGG 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                     computer readable medium has been developed which has recorded on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1517 ACAAAATCAGTACTATGAAAATTGGGAGTTATGTTTAGCAGATGATGCATCGCCAAGCGA 1458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tgatttaaaagcaattcttaacagaatattcagttgtagataatagaataaaaatcttgct 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                        New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
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                                                                                                                         6009900-sn26
                                                                                                                                                             97US-0046655
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               WO9850555-A2
                                                                                                                         14-NOV-1997;
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Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CPG dimucleotides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, graft-versus-host disease, aging, glomerular disease, Lewy body disease, arthritis,
                                                                                                                          Cell cycle; human; CpG dinucleotide; cytosine methylation; HIV; aging; human immunodeficiency virus; neurodegenerative disorder; solid tumour; graft-versus-host disease; glomerular disease; Lewy body disease; cancer; arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic; immunosuppressive; antitumour; cytostatic; antiarteriosclerotic; ds:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Designing primers and probes for analysing diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arteriosclerosis comprising fragments of chemically modified genes associated with cell cycle -
                                                          pretreated genomic DNA associated with cell cycle #45.
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0; Mismatches 458;
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2000DE-1019058.
2000DE-1019173.
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18-DEC-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                      Chemically
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                                                                                       6.7%; Score 63; DB 22; Length 5689;
44.3%; Pred. No. 0.0072;
                                                          Sequence 5689 BP; 1490 A; 207 C; 1277 G; 2707 T; 8 other;
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(EPIG-) EPIGENOMICS AG.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumour suppressor gene; oncogene; antitumour; cytostatic; tumour; CpG dinucleotide; single-nucleotide polymorphism;
                                                                                                                                     aataagaggagetetggetg-attteaaaateggettaeteaataaagtaettttaeagt
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cytosine methylation; ds.
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07-APR-2000;
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                                                                                                                                                                The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genea associated with tumour suppression and concogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may for analysing diseases associated with Cpc dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or thrapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters. The parameters of the compared to another set of genetic and/or epigenetic parameters. The parameters of the compared to another set of genetic and/or prognosis events which are disadvantageous to patients. The present sequence is one of the
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                                                                     tumour suppressor
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                                                                  of chemically modified genes associated with tumour suppi
oncogenes, useful in designing primers and probes for
diseases associated with cytosine methylation state e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                     533 genomic sequences derived from tumour suppressor genes and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.7%; Score 63; DB 22; Length 5689;
14.3%; Pred. No. 0.0072;
ve 0; Mismatches 458; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5689 BP; 1490 A; 207 C; 1277 G; 2707 T; 8 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                          Claim 1; SEQ ID No 148; 27pp; English
             Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this
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             Piepenbrock
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genes and
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                                                                                                                                                                                                                                                                                    glycosyltransferase polypeptides and polynucleotides useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biosynthetic locus; biosynthesis; lipid A biosynthesis; cectyltransferase; Beta-1, 4GalNMc transferas, Beta-1, 3-galactosyltransferase; alpha-2, 3-sialyltransferase; sialic acid synthase; CMP-sialic acid synthetase; mimic; antibody;
                                                                                                            aataagaggagctctggctg-atttcaaaatcggcttactcaataaagtacttttacagt
                                                                                                                                                                                                                              atagattaaacgagaatggaatatcacaaaccaataagtttaagcaatatttactcag
                                                                                                                                                                                                                                                                                                                                             ctattttacaagatttttataaagaaaaatcttatattgatatcacaaaaattactaatt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               actttcaagagtatgtgataaagaaacgctatactcagcaagagctctctaaatattttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campylobacter jejuni beta-1,3-galactosyltransferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunity; immunogen; ganglioside;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CANA ) NAT RES COUNCIL CANADA
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31-JAN-2000; 2000US-0495406.
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                                                          is useful for synthesising slatylated oligosaccharides such as are useful for chemo-enzymatic synthesis of oligosaccharides.

C ganglioside, lysoganglioside or their mimics. Glycosyltransferases are useful for chemo-enzymatic synthesis of oligosaccharides, including gangliosides and other oligosaccharides that have biological activity. The enzymes and nucleic acids that encode them are useful for studies of the pathogenesis mechanisms of organisms that synthesize ganglioside mimics, such as C. jejuni and the nucleic acids are used as probes to study expression of genes involved in ganglioside mimetic synthesis. Antibodies raised against the glycosyltransferases are also useful for analyzing the expression patterns of these genes involved in pathogenesis. The oligonucleotides for inhibiting expression of the campylobacter oligonucleotides for inhibiting expression of the campylobacter canzymes that are involved in the biosynthesis of ganglioside mimics that can mask the pathogens from the host's immune system. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300
                                                                                                                                                                                                                                                                                                             oligosaccharides are useful as diagnosing reagents or as therapeutics and as immunogens for producing antibodies. Bacterial glycosyltransferase can be used to catalyse the formation of
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                                               A reaction mixture for the synthesis of a sialylated oligosaccharide
                                                                                                                                                                                                                                                                                                                                                 oligosaccharides that are identical to the corresponding mammalian structures and are easier and less expensive to produce in large quantity, compared to the mammalian glycosyltransferase. The bacterial origin of the enzymes facilitates expression of large quantities of the enzymes using relatively inexpensive prokaryotic expression systems.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 atttctaagggagaatatattttagaatggatgctgatgatatttcatatccaagtaga
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51.2%; Pred. No. 0.02;
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0; Mismatches 156;
               Disclosure; Page 103; 120pp; English,
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Best Local Similarity 51.23
Matches 167; Conservative
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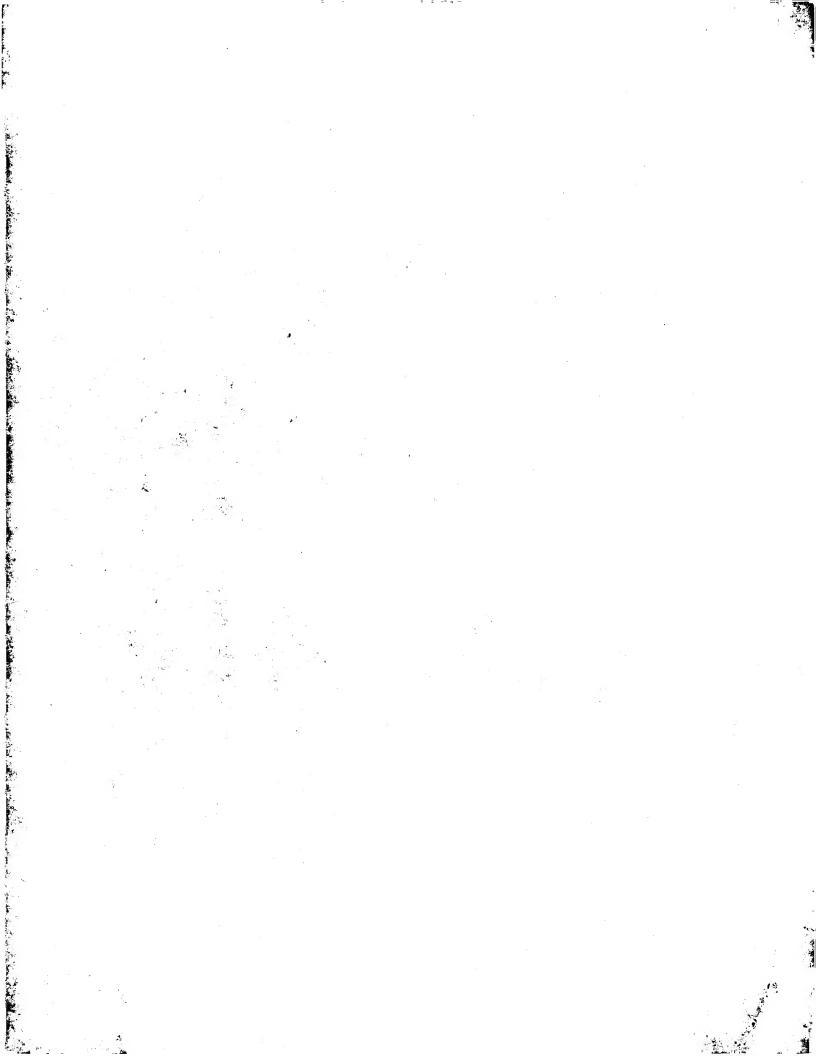
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The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretracted DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and concedence having a sequence taken if trom 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences complementary to (Ss). The nucleic acid may be a complementary to (Ss). The nucleic acid may be a complementary to (Ss). The nucleic acid may be compart of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an carray for analysing diseases associated with cpc dinucleotides e.g. cancers and tumours. The probes can also be used in a method for a scertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The praemeters may be compared to another set of genetic and/or epigenetic parameters which as differences serving as basis for diagnosis and/or prognosis events which are disdivantageous to patients. The present sequence is one of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oncogenes, useful in designing primers and probes for diseases associated with cytosine methylation state e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 7814;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7814 BP; 1677 A; 101 C; 1779 G; 4257 T; 0 other;
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46.6%; Pred. No. 0.021;
iive 0; Mismatches 221;
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07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
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Search completed: August 2, 2002, 13:32:33 Job time: 4229 sec



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Perfect score:
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Issued_Patents_NA:*
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2: /cgn2_C/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_C/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_C/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_C/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_C/ptodata/2/ina/PcTUS_COMB.seq:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result		Query	:		*	
ON :	Score	Match	Length	e :	ID	Description
υ	1 56.6	6.0	19124	~	US-08-487-826B-13	Sequence 13, Appl
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υ	3 51	5.4	854	4	US-08-998-416-534	534,
υ	4 50	5.3	860	4	US-08-998-416-287	287,
	5 50	5.3	6124	4	US-08-213-419B-3	3, A
υ	6 49.4	5.3	7218	-	US-08-232-463-14	14
	7 48.8	5.2	1882	٦	US-08-257-073-12	12,
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44.000000000000000000000000000000000000	T 1 -487-8268-13/C uence 13, Application U NERAL INFORMATION: APPLICANT: Sim, Kim L. APPLICANT: Chitnis, Ch APPLICANT: Chitnis, Ch APPLICANT: Miller, Lou APPLICANT: Miller, Lou APPLICANT: Wellems, Th TITLE OF INVENTION: BI TITLE OF INVENTION: AN NUMBER OF SEQUENCES: 4 CORRESSEE: Knobbe Ma STREET: 620 Newport Beach STREET: 621 Newport Beach STREET: G11 Fornia COUNTRY: US STREET: G20 Newport CITY: Newport Beach STREET: G20 Newport COMPUTER: LOPPY COMPUTER: LBM PC com OPERATING SYSTEM: PC SOFTWARE: PATCATION DAT APPLICATION NUMBER: FILING DATE: 10-SEP CLASSIFICATION: 435 ATTORNEY/AGENT INFORMAT NAME: ISTARION NUMBER: FELEPHONE: (619) 235 TELEFAN: (619) 235 TYPE: NUCLEIS TONE TOPPLOCKET INDEA TYPE: NUCLEIS TONE MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANT: SENSE: NO AND ANT: SENSE: NO ANT: SENSE: NO ANT: SENSE: NO ANT: SENSE: NO AND ANT: SENSE: NO AND AND AND AND AND AND AND A	
444444444444444 0	TILICATION: ISM, KIMINION: ISM, KIMINION: ISM, KIMINION: ISM, CALLON: ISM, CALLON	
	T 1 -487-826B-13/C uence 13, Applic uence 13, Applic uence 13, Applic uence 13, Applic APPLICANT: Sim, APPLICANT: Sim, APPLICANT: Sim, APPLICANT: Sim, APPLICANT: Well CONDUTES: ESOURNE CONDUTER: Califo COUNTRY: US STREET: Califo COMPUTER: BM COMPUTER: BM APPLICATION NU FILING DATE: COMPUTER: BM COMPUTER: BM APPLICATION NU FILING DATE: COMPUTER: BM COMPUTER: BM COMPUTER: BM APPLICATION NU FILING DATE: COMPUTER: BM COMPUTER: BM COMPUTER: BM ATTORNEY/AGENT IN NAME: ISTRATION NU FILING DATE: CLASSIFICATION TELEPHONE: (619 TELEFAX: (619 TELEF	
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Newport Beach California

OF SEQUENCES:

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SOFTWARE PATENTIN STIEM:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 10-SEP-1993

CLASSIFICATION: 435

ATTONREY/AGBRT INFORMATION:

NAME: 12FABLSCH, Ned

REGISTRATION NUMBER: 29,655

REGISTRATION NUMBER: 29,655

REGISTRATION NUMBER: 29,655

REGISTRATION NUMBER: 29,655

REGISTRATION NUMBER: 01,01CP1

TELEPHONE: (619) 235-8550

TELEPHONE: (619) 235-8550

TELEPHONE: (619) 235-0176

INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
             CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
HYPOTHETICAL: 1
                                                                                                                                  ZIP: 92660
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US-08-487-826B-13
                                                                                                              COUNTRY:
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 NO.
 Pred.
43.68;
Best Local Similarity 43.6
Matches 363; Conservative
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                               0; Mismatches 474;
Score 55.6; DB 2;
Pred. No. 0.0012;
Query Match 5.9%;
Best Local Similarity 42.5%;
Matches 351; Conservative
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Sequence 13, Application US/08487826B
Patent No. 5993827
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Miller, Louis H.
APPLICANT: Natler, Louis H.
APPLICANT: Su, Xin-zhaun
APPLICANT: Su, Xin-zhaun
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS

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APPLICANT: Philipl
APPLICANT: Pohlman
APPLICANT: Steine:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-998-416-287/C
; ORGANISM:
US-08-998-416-534
                                                                                                                                                                                              101
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694 aaagaaaaat cttatattgatatcacaaaaattactaattacttcaagagtatgtgat 752
                                                 atatcacaaaccaataagtttaagcaatatatttactcagctattttacaagatttttat
                                                                                                                                                                             753 aaagaaacgetataeteccageaagagetetetaaatattttgagetaaaatetaeeectag
                                                                                                                                                                                                                                               tattactattagaaaactatatttgtttatattttatactttaagtctcccttggttag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Philippsen, Peter
APPLICANT: Steiner, Sabine
APPLICANT: Steiner, Sabine
APPLICANT: Steiner, Sabine
APPLICANT: Wendland, Jurgen
APPLICANT: Wenchtle, Philipp
APPLICANT: Rebisching, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                    873 gaggttattaataaatgatattaatattttagtactgaaattgttt 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 919-541-8587
TELEFRAX: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: NO. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/OB/998,416
FILING DATE: 24-DEC-1997
CLASSIFRICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 534, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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ORIGINAL SOURCE:
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161 cagttgtagataatagaataaaaatcttgcttaatgaagaaaatattggtttagcatcaa 220
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                                                                                                                        41 taaattatgtgagagattcagtagaatctatattaaatcaaacgcttactgattttgagt 100
                                                                                                                                                                             649 TAAAATAAATAGAAACCATAAGTTAATTGATTCATAAAGAAAATGGAATTATTGTGGCA 590
                                                                                                                                                                                                                                           tcataattgtcattgataatccaagtagaggtgatttaaagcaattcttaacagaatatt 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr. Christine
APPLICANT: Mont, Christine
APPLICANT: Mendland, Jurgen
APPLICANT: Rectile, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENONIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No 6239264artis Corporation
                                                             5
   Length 854;
                                                             Indels
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Pred. No. 0.0072;
0; Mismatches 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 287, Application US/08998416 ; Patent No. 6239264
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CITY: Research Triangle Park
Query Match 5.4%;
Best Local Similarity 45.1%;
Matches 265; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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GENERAL INFORMATION:
APPLICANT: Inselburg, J. et al.
TITLE OF INVENTION: GENE ENCODING PROTEIN ANTIGENS OF PLASMODIUM FALCIPARUM
TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2529 ataattattatataaataaataatatatttttacgcatacacaaacatttgtcattat 2588
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Pred. No. 0.016;
0; Mismatches 255; Indels
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                                                                                                                                                                                                          FILE REFERENCE: JII-002CNCP
CURRENT APPLICATION NUMBER: US/08/213,419B
CURRENT FILING DATE: 1994-03-14
PRIOR APPLICATION NUMBER: US 07/870,506
PRIOR FILING DATE: 1992-04-17
                                                                          Sequence 3, Application US/08213419B Patent No. 6333406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14, Application US/08232463 Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.3%;
Best Local Similarity 44.3%;
Matches 203; Conservative 0
                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO SEQ ID 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | LCCATION: (2407)...(2439)
| NAME/KEY: CDS
| LOCATION: (2598)...(3404)
| NAME/KEY: CDS
| LCCATION: (3580)...(3720)
| NAME/KEY: CDS
| LCCATION: (3850)...(5835)
| US-08-213-419B-3
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                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 aatatatttttagaatggatgctgatgatatttcatatccaagtagatttgataagcaaa 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 ttcgttt-tatggaggaaaattcattggatttctcagcaactctaatagaattgatagac 372
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COMPUTER: IBM PC COMPAGEDOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
                                                                                                                                                                                                                                                        NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REGISTRATION NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFRAX: 919-541-8689
                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 287: SEQUENCE CHARACTERISTICS: LENGTH: 860 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tatagattaaacga 626
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526 TIAAAAGAIGGAGGIITIIGCIITIICCICCAACAGAACCICITAIGICACCAAIGACAITA 585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 gtagataatagaataaaaatcttgcttaatgaagaaaatattggtttagcatcaagtttg 225
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                                                             1042 CCAAGCTCGGAATTAATTCTGTGAGCGTATGGCAAACGAAGGAAAAATAGTTATAGTAG 984
                      483 cgtaaaaaagaaagttttcgataagttaatgggatatagagatttagtacctgttgaag
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                                                                                                                                                                                                                                APPLICANT: de Taisne, Charles
APPLICANT: de Taisne, Charles
APPLICANT: Tine, John A.
TTLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue, 25th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 48.8; DB 1;
Pred. No. 0.024;
0; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERNCE/DOCKET NUMBER: 454310-2570
TELECOMMONICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/075,783
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/852,305
FILING DATE: 18-MAR-1992
PRIOR APPLICATION NUMBER: US 07/672,183
FILING DATE: 20-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       New York
: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/257,073
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                         Sequence 12, Application US/08257073 Patent No. 5766597 GENERAL INFORMATION:
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TELEFAX: (212) 840-0712
TELEX: 42506 CURMS
INFORMATION FOR SEQ ID NO: 12:
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ilarity 47.4%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Matches 146; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 09 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UN
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US-08-257-073-12
                                                                                                                                 RESULT 7
US-08-257-073-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 aatcttgcttaatgaagaaaatattggtttagcatcaagtttgaacaaagcggtgaaaat 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 ttctaagggagaatatattttagaatggatgctgatgatatttcatatccaagtagatt 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 tgataagcaaattcgttttatggaggaaaattcattggatttctcagcaactctaataga 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       attgatagaccaaaaaggaaatttagtatataaacaacgagaaagtaataaaatatactt 422
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                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                  APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
CORRESPONDENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY, AGGNT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMM
TELECOMMUNICATION INFORMATION:
TELECHONE: (703)836-9300
                                                                                                                                                   E: Foley & Lardner
1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                      ZIP: 22313-0299
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-232-463-14
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GENERAL INFORMATION
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                                                                                                                                                                                                                                           USA
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                                                                                                                                                                  286 tcatatccaagtagatttgataagcaaattcgttttatggaggaaaattcattggatttc 345
                                                                                                                                                                                          346 tcagcaactctaatagaattgatagaccaaaaaggaaatttagtatataaacaacgagaa 405
                                                                                                                                                                                                                                                                                           706 TATCCAGCTGTTTATGATGACAAAGATAAAAGTGTCATATATTATATTGCAGCTCAA 765
  166 gtagataatagaataaaaatcttgcttaatgaagaaaatattggtttagcatcaagtttg
                                                                                                                      586 GATGAAATGAGACATTTTTTATAAAGATAATATATGTAAAAAATTTAGATGAATTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wohr, Christine
APPLICANT: Wohl, Christine
APPLICANT: Wandland, Jurgen
APPLICANT: Reachtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 622201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/998,416 FILING DATE: 24-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 186, Application US/08998416
Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38,241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS:
LENGTH: 615 base pairs TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                      406 agtaataa 413
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US-08-998-416-186
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                                                                                                       tcatatccaagtagatttgataagcaaattcgttttatggaggaaaattcattggatttc 345
                                       646 TTATGTTCAAGACATGCAGGAAATATGATTCCAGATAATGATAAAAATTCAAATTATAAA 705
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                                                                              346 tcagcaactctaatagaattgatagaccaaaaaggaaatttagtatataaaacaacgagaa
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                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: de Talsne, Charles
APPLICANT: Tine, John A.
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 48.8; DB 1; Length 1:
Pred. No. 0.024;
0; Mismatches 162; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PPLICATION UNBER: US/08/257,073 FILING DATE: 09-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: Curtis, Morris & Safford, P.C. 530 Fifth Avenue, 25th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 454310-2570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNBER: US 08/075,783
FILING DATE: 11-UNN-1993
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/852,305
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/872,183
FILING DATE: 20-MAR-1997
FILING DATE: 20-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08257073
Patent No. 5766597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066 CURTMS
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Frommer, William S. REGISTRATION NUMBER: 25,506
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 47.43
Matches 146; Conservative
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US-08-257-073-8
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                               RESULT 11
US-08-998-416-288/c
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              Best Local Sim
Matches 116;
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COUNTRY:
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                              636 atcacaaaccaataagtttaagcaatatatttactcagctatttacaagatttttataa 695
                                                                                                                                                                                                                                                        491 ATAAGAAATTAAAGTTAAAATTAATTATTAATAATTCTTATAAAAAGTTAAATAATAT 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 195, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
          Score 48.6; DB 4; Length 615;
Pred. No. 0.022;
0; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER REDABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM MSDOS VERSION 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Genome Sciences, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Human Genome Sclen
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 195:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    311 TATATTAATTATTGATAAT 293
          tch 5.2%; sal Similarity 49.2%; 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  876 gttattaataaatgatatt 894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 844 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                                                                              223 ttgaacaaagcggtgaaaatttctaagggagaatatattttagaatggatgctgatgat
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APPLICANT: Steiner, Sabine
APPLICANT: Wohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
CORRESPONDENCE ADDRESS:
Length 844;
                                                                                                                                                                                                                                                                                                                                                                                            283 atttcatatccaagtagatttgataagcaaattcgttttatggaggaaaa 332
                                                                                                                                                                                                                                                                                                                                                                                                                                         224 ATCGTAAAAGAAAATATGATTGAAACTCTTTATCAGCAAGTCCAAGAAA 273
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/999,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
Score 47.6; DB 3;
Pred. No. 0.039;
0; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF/5-30306/A/CGC1976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 288, Application US/08998416
Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
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Research Triangle Park
No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF,
TELECOMMUNICATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 919-541-8689 .
INFORMATION FOR SEQ ID NO: 288:
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APPLICANT: Philippsen, Peter
  5.18;
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                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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US-08-998-416-288
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31,392
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                                                                                                      LENGTH: 3701 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                   Best Local Similarity 46.3
Matches 151; Conservative
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 6300 Colum
CITY: Seattle
STATE: Washington
                                                                                                                                                        linear
                                                                                                                                     STRANDEDNESS:
TOPOLOGY: lir
US-08-845-258-10
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APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                             Length 837;
                         Score 47.4; DB 4; Length 8 Pred. No. 0.043; 0; Mismatches 296; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              811 agtattactattagaaaactatatatttgtttatatttata 851
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APPLICATION NUMBER: US/08/845,258 FILING DATE: 24 APR-1997 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                           5.0%;
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NAME: Maki, David J.
                                                            Conservative
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                                           Similarity
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US-08-845-258-10/c
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                                                          Matches 225;
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CITY: Se
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                           Query Match
Best Local 9
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GENERAL INFORMATION:
APPLICANT: Reed, Steven G. et al.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: SEED AND BERRY 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 175;
REFERENCE/DOCKET NUMBER: 210121,426C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                    4.9%; Score 46; 46.3%; Pred. No.
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; Sequence 10, Application US/08990571
; Patent No. 6214971
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ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
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(206)682-6031
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ADDRESSEE: No. 62392
                                                                                                          ; TOPOLOGY: linear
US-08-723-142A-10
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                    Gaps
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US-08-723-142A-10/C
Sequence 10, Application US/08723142A
Sequence 10, Application US/08723142A
Sequence 10, Application US/08723142A
Sequence 10, Application:
APPLICANT: Reed, Steven G.
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Steath, Paul R.
TITLE OF INVENTION: COMPOURDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
TITLE OF SEQUENCES: 49
                                                                                                                                                                                DB 4; Length 3701;
                                                                                                                                                                              Score 46; DB 4; Length 370 Pred. No. 0.11; 0; Mismatches 175; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6300 Columbia Center, 701 Fifth Avenue
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PELLING DATE: 01-0CT-1996

CLASSIFICATION: 536

ATTORNEY AGENT INFORMATION:
NAME: MAKI, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.426

TELECOMUNICATION INFORMATION:
TELECHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ttaatattttagtactgaaattgttt 918
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Cent
           INFORMATION FOR SEQ ID NO: 10.
SEQUENCE CHARACTERISTICS:
LENGTH: 3701 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                              4.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
(206)682-6031
                                                                                                                                                                                                 Best Local Similarity 46.3
Matches 151; Conservative
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STATE: Washington
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US-08-990-571-10
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TELEFAX:
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                                                                                                                                                                                                                                                                                                                              593 tcaataaagtacttttacagtatagattaaacgagaatggaatatcacaaaccaataagt 652
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
                                                                                                                                                                                                                                                                             0; Mismatches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No. 6239264artis Corporation
                                                                                                                                                                                                                              Score 46;
Pred. No. (
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TITLE OF INVENTYON: GENOWIC DNA SEOU
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             893 ttaatattttagtactgaaattgttt 918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1137, Application US/08998416 Patent No. 6239264 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
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T: Pohlmann, Rainer
T: Steiner, Sabine
T: Mohr, Christine
T: Wendland, Jurgen
T: Knechtle, Philipp
  10:
                                                                                                                                                                                                                            Query Match 4.9%;
Best Local Similarity 46.3%;
INFORMATION FOR SECTED NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 3701 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8689
INFORMATION FOR SEQ ID NO: 1137:
SEQUENCE CHARACTERISTICS:
LENGTH: 636 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDENNESS: Single
                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1692RP
US-08-998-416-1137
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Search completed: August 2, 2002, 13:28:36 Job time: 9682 sec

us-09-900-038a-1.rsp

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 31, 2002, 18:56:25; Search time 13.52 Seconds Run on:

(without alignments) 896.392 Million cell updates/sec

US-09-900-038A-1

score: Perfect

1590 1 MNYSIIMSVYNEPLNYVRDS......LINDINILVLKLFGGEKQSD 313 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	457		Q48215 haemophilus	ıΔ	_	P46918 bacillus su	Q57022 haemophilus	-	_	P77414 escherichia	ร	4	6	_	Q46632 erwinia amy	~	Q9wu83 cricetulus	Q50587 mycobacteri			6						P25805 plasmodium	Q54865 streptococc	P25239 escherichia	97	34	buchnera	051578 borrelia bu
SUMMARIES	DI	YA57_METJA	YF78_HAEIN	YG95_HAEIN	AMSE_ERWAM	YG96_HAEIN	GGAB_BACSU	Y868_HAEIN	YIBD_ECOLI	SPSA_BACSU	WCAA_ECOLI	Y4G1_RHISN	YWDF_BACSU	YS86_ANASP	YKCC_BACSU	AMSB_ERWAM	DPM1_MOUSE	DPM1_CRIGR	YF20_MYCTU	DPM1_HUMAN	Y208_BORBU	DPOM_PODAN	GGAA_BACSU	P115_MYCHR	HMW2_MYCGE	DPM1_SCHPO	NISB_LACLA	CYSP_PLAFA	HASA_STRPY	T257_ECOLI	HFA1_YEAST	MTS1_STRSA	Y087_BUCAI	EX5B_BORBU
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df	Query Match	27.5	16.6		12.5		12.	11.9		•		10.0	9.1	9.1	8.8	8.1	7.9	7.7	7.7	7.5	7.5	7.5	7.4			•						٠	6.9	٠.
	Score	3	264	206.5	199.5	196.5	192	189	182.5	175	161	158.5	145	144.5	140	129	125	123	122.5	119	119	119	118	116.5	_	4	113.5	113	112	110.5	-	109.5	109	107
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Januachtt.
Science 273:1058-1073(1996).
-i- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.

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Length 290;

InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Complete proteome.
SEQUENCE 290 AA; 35099 WW; 3F6A1B221C420D74 CRC64;

EMBL; U67549; AAB99061.1; -. HSSP; P39621; 10G8.

MJ1057

64 LNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEEN-SLDFSATLIEL 122

27.5%; Score 437.5; DB 1; 35.2%; Pred. No. 1.7e-22; tive 58; Mismatches 101;

Conservative

Query Match Best Local Similarity Matches 99; Conserv

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Y060_MYCPN EXOU_RHIME EXOU_RHIME EXOU_RHIME EXOU_RHIME EXOU_BOLOAL CSBB_BACSU CSBB_BACSU SYL_YEAST CSTD_BACSU BPS2_ACIAM MOTL_BORBU P32985 acidianus a MOTL_BORBU P32767 saccharcomyc P56785 arabidopsis YFRE_MYCTU Q50864 myxococcus	T 1 METJA METJA METJA STANDARD; PRT; 290 AA. 058457; METJA STANDARD; PRT; 290 AA. 15-JUL-1998 (Rel. 36, Created) 16-OCT-2000 (Rel. 39, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Putative glycosyl transferase MJ1057 (EC 2). Methanococcus jannaschii. Archaea: Euryarchaeota; Methanococcaees; Methanococcus.	NCBI_TaxID=2190; [1] SEQUENCE FROM N.A. SEQUENCE 5337999; Dubmed=8688087; Bult C.J. White O. Olsen G.J. Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Radich G.I., Overbeek R., Kirkness E.F., Weidnan JF., Adams M.D., Radich C.I., Scott J.L., Geoghagen N.S.M., Weidnan J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk HP., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; "Complete genome sequence of the methanogenic archaeon, Methanococcus Schance 273:1058-1073/1996.
299 342 1070 1070 1104 426 582 582 610 1081 1786 319	STANDARD: 1. 36, Created) 1. 39, Last seq 1. 40, Last ann yl transferase annaschii.	NCBI_TaxID=2190; NCBI_TaxID=2190; SEQUENCE FROM N.A. STRAIN=JAL-1 / DSM 2661 / ATCC 43067; MEDLINE=96337999; Pubmed=868087; Bult C.J., White O., Olsen G.J., Zhou Sutton G.G., Blake J.A., FitzGerald L. Kerlavage A.R., Dougherty B.A., Tomb Overbeek R., Kirkness E.F., Weinstock Scott J.L., Geoghagen N.S.M., Weidman Utterback T.R., Kelley J.M., Peterson Cotton M.D., Roberts K.M., Hurst M.A., Cotton M.D., Roberts K.M., Amith H.O., "Complete genome sequence of the methalannass and schools of the
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106.5 106.5 106.5 104.5 104.5 104.1 104.1 104.1 103.5 102.5	T 1 XA57_METJA STANDARD; CS8457; 15-JUL-1998 (Rel. 36, Cr 30-MAY-2000 (Rel. 39, La 16-OCT-2001 (Rel. 40, La Putetive glycosyl transf MJ1057. MATOBA RELYARCHAROSCOLUS ACCHAROSCOLUS MATOBA RELYARCHAROSCOLUS METHANOCOCCUS	NCBI_TaxID=2190; [1] SEQUENCE FROM N.A. STRAIN=JAL-1 / DSM STRAIN=JAL-1 / DSM STRAIN=JAL-1 / DSM STRAIN=JAL-1 / DSM Bult C.J., White O Sutton G.G., Blake Kerlavage A.R., Do Overbeek R., Kirkn Scott J.L., Geogha Utterback T.R., Ke Cotton M.D., Rober Klenk HP., Frase "Complete genome s "Complete genome s "Complete genome s
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DFWIRCIANDYKFDIIEEFLLKYRIPNRDNYLSRIKKOKLYSYYT-LKTHWKNKKHFCNN 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE—95350630; PubMed=7542800; Playton R.A., Kirkness E.F., Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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                                                                       DFAIRGALADFKIGLLNKVLLQYRL--NENGISQTNKFKQYIYSAILQDFYKEKSY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 269:496-512(1995).
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 323;
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Pfam: PF00535, Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7CBC2681039AB5B4 CRC64;
                                                                                                                                                                                                                                                                                                       YF78_HAEIN STANDARD; PRT; 323 AA. Q57287; 005077; 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1998 (Rel. 36, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Putative 91ycosyl transferase H11578 (EC 2.-.-).
                                                                                                                                                                                                                     248 VYFWKV--FFYSLVV------YLFIVLTPTFILKIL 275
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Pred. No. 6.5e-11;
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29.0%;
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Matches 93; Conserv
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Whole-genome random sequencing and assembly of Haemophilus influenzae
66 SNKYNLGFINSLNIGLGGCFSGKYFARMDADDIAKPSWIEKIVTYLEKNDHITAMGSYLEI 125
                                                          175
                                                                                                   185
                                                                                                                                                                                                                                                                   241 ITYYLNKIGIDIKVINSVSLLEIYHVDKSNKVLKSILYEMYMSLDKYTITSLLHFIKYHL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=RD / KW20 / ATCC 51907;
MEDLINE=95350630; bubmed=7542800;
MEDLINE=95350630; bubmed=7542800;
MEDLINE=95350630; bubmed=7542800;
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fitelds C.A., Gocayne J.D., Shirley R. Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Sandek D.M., Brandon R.C., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Venter J.C.,
                                                                                    -DFYKEKSYIDITKITN----SKY--
                                                          IDQKG-NLVYKQRESNKIY----LTNDIRKMLLNRSILAHPTWCVKKKVF--DKLMGYRD
                                                                                                                                       176 LVPVEDYDF----AIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIYSAILQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McLaughlin R., Abu Kwaik Y., Young R., Spinola S., Apicella M.; "Characterization and sequence of the 1sg locus from Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interprio: IPR001173; Glycos_transf_2.
Pfam: PF00535; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Putative glycosyl transferase HI1695 (EC 2.-.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            267 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                              279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       048215; 005081;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last seq
                                                                                                                                                                                                                                                                                                                                                     301 ELFDLKONLKIIKKFIRKINV 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M94855; AAA24983.1; -.
                                                                                                                                                                                                                                                                                                              --FELKSTPSIT---IRKLYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U32842; AAC23341.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus influenzae
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Pred. No.

Best Local Similarity

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                                                                                                                                                                                                                             118 TLIELIDOKGNLV-YKQRESNKIYLTNDIRKMLLNRSILAHPTWCVKKKVFDKLMGYRDL 176
                                                                                                                       Gaps
                                                                                                                                                                                                            60 IKILLNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEEN--SLDFSA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bugert P., Geider R.; ^{\prime} Molecular analysis of the ams operon required for exopolysaccharide
                                                                                                                                                  1 MNYSIIMSVY-NEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNR
                                                                                                                                                                                1 MKFSVLMSLYIKENPQFLRECFESLVAQTRQADEIVLVFDGVVTPDLEFVVTEFE-TKLP
                                                                                                                                                                                                                                                                                           177 VPVEDYDFAIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIYSAILQDFYKEKSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NoV-1997 (Rel. 35, Created)
01-NoV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Amylovoran blosynthesis glycosyl transerase amsE (EC 2.-.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001173; Glycos_transf_2.
Pfam: PF00535; Glycos_transf_2; 1.
Exopolysaccharide synthesis; Transferase; Glycosyltransferase.
SEQUENCE 266 AA; 30748 MW; 163268A4210EB47B CRC64;
                                                                                        Length 267;
                                                                                                      Pred. No. 3.4e-07;
57; Mismatches 130; Indels
V -> G (IN REF. 1).
D -> E (IN REF. 1).
F -> S (IN REF. 1).
A2F1A0532737DBC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              IDITKITNYFQEYVIKKRYTQQELSKYFELKSTPSITIRKLY 278
                                                                                                                                                                                                                                                                                                                                                                                                                          LGIQGLLSGLFTFALR ------FGSRLLPTSLLKKLY 261
                                                                                         DB 1;
                                                                                      13.0%; Score 206.5; 24.8%; Pred. No. 3.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-9531933; PubMed-7596293;
26 V
46 D
49 F
30770 MW;
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                                                                                                                    70; Conservative
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26
46
49
267 AA;
                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amylovora
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Q46635;
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CONFLICT
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SEQUENCE
                                                                                         Query Match
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DB 1; Length 266;

Score 199.5;

12.5%;

Query Match

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                    12;
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                                                                                                                                                                                                                                                  AAVIEFDEHG----KERLKRLPLSNNDIHEFARMKNPFNH--MCV----VFRKDKVISAGS 168
                                                                                                                                                                                                                                                                                                                           61 KILL--NEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEEN-SLDFSA 117
                                                                                                                                                                             PLVIVPLEKNLGLGKALNAGLERCTHNVVARMDTDDICLPERFEKQISYMESHPEVVLSG 117
                                                                                                                                                                                                                     118 TLIELIDQKGNLVYKQRESNKIYLTNDIRKMLLNRSILAHPTWCVKKKVF--DKLM---G 172
                                                                                                                                                                                                                                                                                                  173 YRDLVPVEDYDFAIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIYSAILQDFYK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-9550630; PubMed-7542800; Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M., McKenlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fitchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Venter J.C., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                       Gaps
                                                          YSIIMSVYN--EPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVDNRI 60
                                                                                                57
                                                                                 2 FSVLISLYNKEKPEN-LEQCLESLHQQTLNADEIVLYYDGPVSESLKAVATRWA---NLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McLaughlin R., Abu Kwalk Y., Young R., Spinola S., Apicella M.; "Characterization and sequence of the lsg locus from Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
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                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Putative glycosyl transferase H11696 (EC 2.-.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 107;
9.9e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                  48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YG96_HAEIN STANDARD;
04821, 005082;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M94855; AAA24982.1; -. EMBL; U32842; AAC23342.1; -.
28.48;
                                                                                                                                                                                                                                                                                                                                                                                  233 EKSYIDIT --- KITNYF 246
                                                                                                                                                                                                                                                                                                                                                                                                                       226 LKLALKQTGFIRGTLYF 242
                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE FROM N.A.
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YG96_HAEIN
                    Matches
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228 QDFYKEKSYIDITKITNY -----FQEYVI------
  or send an email to license@isb-sib.ch)
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Science 269:496-512(1995).
                                                                                                                                         Query Match
Best Local Similarity 23.79
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294 LINDINILVLK 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     353 SDOTLTIEILE 363
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Y868_HAEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN THE BIOSYNTHESIS OF GALACTOSAMINE-CONTAINING MINOR TEICHOIC ACIDS.
                                                                                                                                                                                                                                                                                                               60 IKILLNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEEN---SLDFS 116
                                                                                                                                                                                                                                                                                                                              117 ATLIELIDOKGNLVYKQRESNKIYLTNDIRKMLLNRSILAHPTWCVKKKVFDKLMGYRD- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 TOKAIDYIREHYVKTVEQARNF-DIN--ASYILAYPHIMNLSRKAAKYYFDIFKKTKSI- 270
                                                                                                                                                                                                                                                                            3 SIIVPSYNRKAE-VPALLESLTQQTSSNFE-VIJVDDCSK------ERVVVEGSYSFP 52
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                             4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNR---- 59
                                                                                                                                                                                                                                                                                                                                                                                113 PAKCEMVNEGFTYVTQPIEPQEI----STERILLANKIGGMPMIAIKKEMFLKIGGLSTA
                                                                                                                                                                                                                                                                                                                                                                                                                                     LVPVEDYDFAIRGALADFKIGLLNKVLLQ-----YRLNE------NGISQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 TNKFKQYIYSAILQDFYKEKSYIDITKITNYFQEYVIKKRYTQQELSKYFEL-KSTPSIT
                                                                                                                                                                                                                                     67;
                                                                                                                                                                                                           Score 196.5; DB 1; Length 294; Pred. No. 1.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
                                                                                                                                                                                                                                     Indels
                                                C -> Y (IN REF. 1).

S -> R (IN REF. 1).

T -> A (IN REF. 1).

C -> R (IN REF. 1).

C -> R (IN REF. 1).

V -> I (IN REF. 1).

V -> I (IN REF. 1).

I -> V (IN REF. 1).

B -> S (IN REF. 1).

B -> S (IN REF. 1).
                .transf_2; 1.
Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                    Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Minor telchoic acids biosynthesis protein ggaB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                900 AA
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NCBI_TaxID=1423;
IPR001173; Glycos_transf_2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274 IRKLYICLYLYFKSPLVRRLLIN 296
                                                                                                                                                                                                          12.4%; Sc
ilarity 25.1%; Pr
Conservative 60;
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(Rel. 32, Last sequ
(Rel. 40, Last anno
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            Pfam; PF00535; Glycos_transf
Hypothetical protein; Transf
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                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 81; Conserv
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                                     Complete proteome
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01-NOV-1995
16-OCT-2001
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P46918;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 SATLIELIDQKGNLVYKQRESNKIYLTN--DIRKMLLNRSILAHPTWC----VKKKVFDK 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 DIVAIPIFFAEGR-TGEHNLNNKFSSTRILDVEKE--PHHILTH---CCSTFIKKDALKN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 IRFDENCKIGEDAKLVNLIISQKKKYGLVKEAKYHYRVREDGSSAMOTAKANKNWFNHSL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 QELSKYFE---LKSTPSITIRKLYICL---------YLYFKSPLVRRL 293
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 NYSIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVI----DNPSRGDL--KQFLTEYSV 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-95350630, PubMed=7542800;
Relarange A.R., Bult C.J., White O., Clayton R.A., Kirkness E.F.,
Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Sprigss T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fricchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LMGYRDLVPVEDYDFAIRGALADFKIGLLNKVLLQYRLNENGIS--QTNKFKQYIYSAIL
                                                                                                                                                                                                                                                                                                                                                                                                       84;
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Haemophilus.
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                                                                                                                                                                                                                                                                                                                               Length 900;
                                                                                                                                                                                                                                                                                                                               12.1%; Score 192; DB 1; Length 90 23.7%; Pred. No. 1.4e-05; Live 69; Mismatches 130; Indels
EMBL; U13979; AAA73513.1; -.
EMBL; Z99122; CAB15585.1; -.
Subtinist; BG11192; ggaB.
InterPro; IPROIT3; G170cs_transf_2.
Pfam; PF00535; G1ycos_transf_2: 1.
Transferase; G1ycosyltransferase; Complete proteome.
SEQUENCE 900 AA; 107154 WW; FA66495488C2C62F CRC64;
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2011 (Rel. 40, Last annotation update)
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Fri Aug

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SPSA_BACSU
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                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIR-KI2 / MG1655.
STRAIR-KI2 / MG1655.
SOFIA H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
"Analysis of the Escherichia coli genome. V. DNA sequence of the
region from 76.0 to 81.5 minutes 1.
Nucleic Acids Res. 22:2576-2586(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 DQKGNLVYKQRESNKIYLTNDIRKM----LLNRSILAHPTWCVKKKVFDKLMGYRDLVPV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 MTHGNYAFCDLEGNQIKLVTTSKKIDYLTLLQGNQFKIMTVLVERESI-KLLRFPN-IKH 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDYDFAIRGALADFRIGLL--NKVLLQYRLNENGISQTNKFKQY1YSAILQDFYKEKSYI 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEENSLDFSATLIELI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-89174812; PubMed-2647748;
Aronson B.D., Somerville R.L., Epperly B.R., Dekker E.E.;
"The primary structure of Escherichia coli L-threonine
dehydrogenase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.9%; Score 189; DB 1; Length 25 27.0%; Pred. No. 4.6e-06; ive 53; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                          Interpro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                28915 MW; A5D8220129782E98 CRC64;
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                                                                                                                                                                                                                                  EMBL; U32768; AAC22526.1; -. HSSP; P39621; 1QG8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68; Conservative
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SEQUENCE 250 AA
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Best Local S
Matches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 -----LLNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEEN 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 ROGNKNLNY--------ORHYIKITRLLEKLNRNYADKIMIYPEFHQQITYEALRVC 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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9 SVIIPLYNAGDDF-RTCMESLITQTWTALEIIIINDGST------DNSVEIA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKI- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 KYYAENYPHVRLLHQANAGASVARNRGIEVATGKYVAFVDADDEVYPTMYETLMTMALED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 --CVKKKV-FDKLMGYRDLVPVEDYDF-AIRGALADFKIGLLNKVLLQYRLNENGIS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 SLDFSATLIELIDOKGNLVYKQRESNKIYLTN-----DIRKMLLNRSILAHPTW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 DLDVAQCNADWCFRETGETWQSIPTDRLRSTGVLTGPDWLRMGLSSRRWTHVVWMGVYRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 -QTNKFKQYIYSAILQDFYKEKSYIDITKI----TNYFQEYVIKKRYTQQ----ELSKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 344;
J. Biol. Chem. 264:5226-5232(1989).
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Transferase; Glycosyltransferase;
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R -> G (IN REF. 2).
9B5DABFE86D5457A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 182.5; DB 1;
; Pred. No. 1.8e-05;
67; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (Rel. 31, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       276 HAVRKEPDILTRQRMIA--EIFTSGMYKRLITN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ecodene; EG11266; yibb.
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2: 1.
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                                                                                                                                                                                                                                                                                                                   EMBL; U00039; AAB18592.1; -.
EMBL; AE000439; AAC76539.1; -.
EMBL; X06690; CAA29885.1; -.
PIR; A30268; Q3ECTH.
PIR; B33276; B33276.
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22.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 74; Conserv
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COLANIC ACID.
                                                                                            NCBI_TaxID=562;
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                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
MEDLINE-92920604; PubMed-10350455;
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"Structure of the nucleotide-diphospho-sugar transferase, SpsA from Bacillus subtlis, in native and nucleotide-complexed forms.";
Biochemistry 38:6380-6385(1999).
-i- FUNCTION: GLYCOSYLTRANSFERASE IMPLICATED IN THE SYNTHESIS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                            6
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Transferase; Glycosyltransferase; 3D-structure; Complete proteome.
NISULPID 155 243
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                                                                                        "Baillus subtilis genome project: cloning and sequencing of the kb region from 325 degrees to 333 degrees."; MOI. Microbiol. 10:371-384(1993).
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Hullo M.F., Ionoscu M., Lubochinsky B., Marcelino L., Moszer I.,
Presecan E., Santana M., Schneider E., Schweizer J., Vertes A.,
Rapoport G., Danchin A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71; Indels 102;
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative colanic acid biosynthesis glycosyl transferase wcaA.
                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
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                                                                                                                                                                                                                                                                                                                                                                  -1- PATHWAY: SPORE COAT POLYSACCHARIDE BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.0%; Score 175; DB 1, 24.6%; Pred. No. 4e-05; iive 45; Mismatches
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Best Local Similarity 24.65
Matches 71; Conservative
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P77414;
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                                                                                                                                                                                                                                                                                            Stevenson G., Andrianopoulos K., Hobbs M., Reeves P.R.;
"Organization of the Escharichia coli K-12 gene cluster responsible for production of the extracellular polysaccharide colanic acid.";
J. Bacteriol. 178:4885-4893(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-K12 / MG1655,
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Rlley M., Collado-Vides J., Glasner J.D., Rode C.K., Maybew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T.,
Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,
Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H.,
Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
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Pfam; PF00535; Glycos_transf_2; 1.
Lipopolysaccharide biosynthesis; Transferase; Complete proteome.
SEQUENCE 279 AA; 33035 MW; 75F74D30026E327A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mau B., Shao Y.;
The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
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                                                                                                                                                                                                                                                             MEDLINE=96326333; PubMed=8759852;
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Bacillus subtilis.
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DYVCQ--GEVYSQPASLPLYPKSPYSRRLFYKRNIIGNQVFTWAWRFKECLFD----TE 175
                                  176 LVPVEDYDFAIRGAL---ADFKIGLLNKVLLQYRLNENGI---SQTNKFKQYIYSAILQD 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE-97305956; Pubmed-9163424;
Fretherg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A., Perret X.;

"Molecular basis of symbiosis between Rhizobium and legumes.";

"Anture 387:394 4001(1997).

-1- SIMILARITY: STRONG TO M.XANTHUS O-ANTIGEN BIOSYNTHESIS PROTEIN RFBC (NOT TO BE CONFUSED WITH ENTEROBACTERIAL RFBC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          474 DAHPDAKIIYTDEDKI-VEGGTRCDAHFKPDWNRDLLYGINYISHLGVFDAALVREVGAF
                                                                     LKAAQDYDIFLRMVVEYGEPWKVEEATQIL---HINHGEMQITSSPKKFSGYFH-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
NCBI_TaxID=394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 909;
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Pfam: PF00535; Glycos_transf_2; 2.
HypothetLcal Protein: Plasain: Pasain: SEQUENCE 909 AA; 102827 MW; 3985D69722F43962 CRC64;
                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 102.8 kDa protein Y4GI.
                                                                                                                            FY-KEKSYID-ITKITNYFQEYVIK-KRYTQQEL 260
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Best Local Similarity
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P55465;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 IVSFEEKNGTRYP--VSRKLFAYTADYEDMRVFSTYV--PSGSMYRRFLHDEIGYFDADV 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W.,
Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I.,
Presecan E., Santana M., Schneider E., Schweizer J., Vertes A.,
Rapoport G., Danchin A.;
"Bacillus subtilis genome project: cloning and sequencing of the
Kb region from 325 degrees to 33 degrees.";
Mol. Microbiol. 10:371-384 (1993).
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X73124; CAA51612.1; -.
EMBL; 299123; CAB15824.1; -.
PIR; S39711; S39711.
Subtilist; BG10602; ywdF.
InterPro; IRR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2, 1.
Hypothetical protein; Transferase; Glycosyltransferase;
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                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                  01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative glycosyl transferase ywdF (EC 2....).
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   268 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254
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STANDARD;
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Best Local Similarity
Matches 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome. SEQUENCE 268 AA;
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P22639;
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YS86_ANASP
ID YS86_AN
AC P22639;
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us-09-900-038a-1.rsp

323 AA

STANDARD;

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AMSB_ERWAM
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        STAN BURKEN BURKEN SCHOOL STAN BURKEN SCHOOL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 GYRDLVPVED------YDFAIRGALADFKIGLENKVLLQYRLN--ENGISQTNK 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-90264305; PubMed-2111805;
Holland D., Wolk C.P.;
"Indentification and characterization of hetA, a gene that acts early
in the process of morphological differentiation of heterocysts.";
J. Bacteriol. 172:3131-3137(1990).
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65; Mismatches 114; Indels
                                                                                                                                     Anabaena sp. (strain PCC 7120).
Bacteria: Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
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Interpro; IPR001173; Glycos_transf_2.
Pfam: PF00555; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase;
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01-AVG-1991 (Rel. 19, Created)
1-AMR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Putative glycosyl transferase alr2836 (EC 2.-.-).
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EMBL; AF031959; AAC32401.1; ALT_INIT.
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=21595285; Pubmed=11759840;
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Best Local Similarity
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RESULT 14 YKCC_BACSU

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InterPro; IPRO01173; Glycos_transf_2.
Pfam; PF0535; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase; Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 ATLIELIDQKGNLVYKQRESNKIYLTNDIRKMLLNRSILAHPTWCVKKKVFDKLMGYRDL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 VVYAVRTKRKGETFFKKQTAAMFYRL------------LSGMTDI 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 VRDERLAGETK-----YPLKK---MLKLSMDGITTFSHKPLKLASYAGILMSGTGFLY 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 -VPVEDYDFAIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIYSAI-----LQDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 YKEKSYIDITKITNYFQEYVIKKRYTQQELS------KYFELKSTPSITIRK---LY
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
NCBL_TaxID=1423;
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                                                                                            15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative glycosyl transferase ykcC (EC 2....).
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YKCC_BACSU STANDARD
034319;
15-JUL-1998 (Rel. 36, C.
15-JUL-1998 (Rel. 36, L.
16-OCT-2001 (Rel. 40, L.
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                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 IELIDQKGN---LVYKQRESNKIYLTNDIRKMLL----NRSILAHPTWC----- 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VKKKVFDKLMGYRDLVPVEDYDFAIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQY 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222 IYSAILQDFYKEKSYIDITKITNY-FQEYVIKKRY-----TQQELS--KYFEL 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KYSLEWLDAMKP----HLTRRDVYTYKAYKLPLRYKMDGKSLQASLSFARYFFL 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48;
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Amylovoran blosynthesis glycosyl transerase amsB (EC 2.-.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Exopolysaccharide synthesis; Transferase; Glycosyltransferase.
EXOPOLYS 301 AA; 34788 MW; 9900E53080E6ECG CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 301;
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Best Local Similarity 21.1%; Pred. No. 0.056;
Matches 62; Conservative 67; Mismatches 117; Indels
                                                                                                                                                            STRAIN-EA1/79;
MEDLINE-9531933; PubMed=7596293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X77921; CAA54883.1; -.
                                                                                                                                             SEQUENCE FROM N.A.
                                                                 Erwinia amylovora
                                                                                                             NCBI_TaxID-552;
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July 31, 2002, 18:51:04 ; Search time 17.53 Seconds (without alignments) 1715.685 Million cell updates/sec
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1 MNYSIIMSVYNEPLNYVRDS......LINDINILVLKLFGGEKQSD 313
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                               OM protein - protein search, using sw model
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Perfect score:
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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

		Description	alveosyl transfera	qlycosyltransferas	qlycosyltransferas	glycosyltransferas	exopolysaccharide	qlycosyl transfera		glycosyl transfera	•	teichuronic acid b	qlucosyltransferas	exopolýsaccharide	biosynthesis of te	hypothetical prote		glyc		glycosyl transfera		minor teichoic aci	lacto-N-neotetraos	glucosyltransferas	hypothetical prote	probable glycosyl	hypothetical prote	probable glycosyl	hypothetical prote	neote	glycosyl transfera
SUMMARIES		ID	H64431	H97167	A97168	B97168	B84114	T44330	G95948	H64130	AG2188	E84107	AB2092	D70036	A69728	E97757	AH2026	E90984	H85829	E71703	G97777	E71690	н81970	AI2091	AG2189	E83022	C64175	G71148	G71153	D81027	F95015
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		Length	290	333	336	333	271	340	367	323	321	257	329	278	252	604	333	260	260	280	281	318	346	343	318	294	267	294	334	349	291
	*	Query Match	27.1	23.1	21.9	19.9	18.9	17.7	17.0	16.6	15.8	വ	3	13.9	m	13.8	13.7	13.7	13.7	13.7	13.6	13.6	13.6	13.4	13.2	13.1	13.0	13.0	12.9	12.9	12.9
		Score	431.5	367	348.5	317	300.5	282	271	264	251	246.5	221.5	221	220	220	218.5	218	218	217.5	216.5	215.5	215.5	212.5	210.5	208	206.5	206.5	205.5	202	204.5
	4 [No.	-	7	٣	4	S	9	7	&	6	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27	28	29

RESULT 2 H97167 glycosyltransferase [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum

glycosyl transfera glycosyl transfera	glycosyltransferas	capsular polysacch	glycosyl transfera	spore coat polysac	glycosyltransferas	galactosamine-cont	glycosyltranserase	hypothetical prote	glycosyltransferas	glycosyl transfera	beta-1,4-galactosy	hypothetical prote	probable glucosylt	hypothetical prote
S70813 H97888	в97189	A70037	B75096	G70036	D64175	E69631	S61898	AH2189	T00090	A64099	T50039	AD1876	E81319	AG2366
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333 1 317 2	268 2	344 2	298 2	344 2	294 2	900 2	258 2	318 2	465 2	250 2	318 2	596 2	274 2	996
12.8 333 1 12.7 317 2														
	12.7	12.6	12.5	12.4	12.4	12.1	12.0	12.0	12.0	11.9	11.8	11.8	11.7	11.7

ALIGNMENTS

MBO PROJERGE PER PROPORTION OF THE PROPORT PRO	H64431 H64431 C;Species: Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 10-Oct-1997 C;Accession: H64431 C;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, Rooc, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.	Science 2/3, 1058-10/3, 1996 Attitle: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc A; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc A; Reference number: A64300; MUID:96337999 A; Reference number: A64300; MUID:96337999 A; Recession: H64431 A; Retaus: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-290 < BUL> A; Residues: 1-290 < BUL> A; Constitues: PID:9159318; TIGR:MJ1057; PIC; Genetics: A; Map position: FOR996513-997385 C; Reywords: 91ycosyltransferase		64 LNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEEN-SLDFSATLIEL 122
	H64431 glycosyl tr C;Species: C;Date: 13 C;Acces: 13 C	lence 2/ Authors: Titlence Reference Accession Status: Molecule Molecule Cross-re Genetics Map posi: Keywords	Query Ma Best Loc Matches 4	Qy 64 Db 71 Qy 123 Db 131 Qy 183 Db 189 Db 237 Db 248

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Page

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C;Accession: B84114
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: B84114
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostridium acetobutylicum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: GB:AE001437; PIDN:AAK80133.1; PID:g15025169; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Bacillus halodurans
C;Date: 01-Dec_2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SRDNNMGMVYSLNEGIDRAKGSYVARMDADDIALPERFERQIEYLNKNKDVDILACKVEA 120
                                                                                                                       64 LNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEEN-SLDFSATLIEL 122
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                                                                                                                                                                                                                                                                 ||||| :| :|| ::||::||:||||| 184 AEDYDLMIRAIRNGYKIVRMECLIKYRVHNKSKTAVEMFNPKMVE-----YTMKAKID 237
                  ISREHRGLVDSLNEGINIARGKYIARMDADDISINNRIEKQFEFLELNKDVDILGTRIEA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---IDQKGNLVYKQRESNKIYLTNDIRKMLLNRSILAHPTWCVKKKVFDKLMGYR-DLVP
                                                                                                                                                                                                                         179 VEDYDFAIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIYSAILQDFYKEKSYID
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1larity 32.8%; Pred. No. 2.6e-13;
Conservative 53; Mismatches 91
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Backeriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                         Solvent-Producing Bacterium Clo
                                                                                       ree
                                                                                   Я.,
C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C; Accession: H97167
R; Molling, J.; Beneton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, J.; Daly, M.J.; Benett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A. Fitle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacter A; Reference number: A96900; MUID:21359325; PMID:21359325
A; Residues: Preliminary
A; Molecule type: DNA
A; Residues: 1-333 < KUR>
A; Residues: 1-333 < KUR>
A; Residues: 1-333 < KUR>
A; Cross-references: GB:AE001437; PIDN:AAK80131.1; PID:q15025167; GSPDB:GN00168
C; Genetics:
A; Gene: CAC2173
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A; Cross-references: GB:AE001437; PIDN:AAK80132.1; PID:g15025168; GSPDB:GN00168
A; Experimental source: Clostridium acetobutylicum ATCC824
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glycosyltransferase [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;C)ate: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: A97168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 VGNISNDI-KEKNENKLNIEFDIYDDNREKILNYWYCLAHPSVMFRKDILRELKGYNDF- 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- QNYEGLKDGI 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 LNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEEN-SLDFSATLIEL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 IDQKGNLVYKQRESNKIYLTNDI----RKMLLNR-SILAHPTWCVKKKVFDKLMGYRDLV 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 333;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 KIKLIDVFKREFKKDFKYIVWGASNGGKITKEVLDEFFE 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 367; DB 2;
; Pred. No. 1.6e-16;
62; Mismatches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.1%;
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les 90; Conserv
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A:Status: preliminary
A:Molecule type: DNA
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Best Local Si
Matches 93;
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Best Local S
Matches 90
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probable glycosyltransferase protein SMb21189 [imported] - Sinorhizobium meliloti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMb21189
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Matches 7
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C; Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C; Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C; Accession: T44330
R; Yamasaki, S.; Shimitu, T.; Hoshino, K.; Ho, S.T.; Shimada, T.; Nair, G.B.; Takeda, Y.
Gene 237, 321-332, 1999
A; Title: The genes responsible for O-antigen synthesis of Vibrio cholerae 0139 are close
A; Title: The genes responsible for O-antigen synthesis of Vibrio cholerae 0139 are close
A; Accession: T44330
A; Accession: T44330
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Ascession: DNA
A; Residues: 1-340 < YAM>A; Residues: 1-340 < YAM>A; Cross-references: EMBL:AB012957; NID:g4115688; PIDN:BAA33634.1; PID:g3721684
A;Molecule type: DNA
A;Residues: 1-271 <STO>
A;Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07433.1; GSPDB:GN0G
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH3714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 DOKGNLVYKORES---NKIYLTNDIRKMLLNRSILA----HPTWCVKKKVFDKLMGYRDL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---GTLAYLFRETPSKNKMMCHPEDHDSLIIRLLFSVCFIHPVVMIRKSVLDQL----DY 172
                                                                                                                                                                                                                                                                                                                                                      LNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEENS-LDFSATLIEL 122
                                                                                                                                                                                                                                                                                                                                                                                            64 HNKNNRGLSYSLAEGVSLAKAPWIARMDADDVSFKDRLAVQMDHVKAHSELDILGSYVID 123
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6 TVLMSVYNDK-NYLSESIESILNQTFENFEFLIINDASTDGS-GELLEEYSKKDKRIRLI 63
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                                                                                                                                                                        ; Score 300.5; DB 2;
; Pred. No. 2.3e-12;
41; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.7%; Score 282; DB 2; 36.9%; Pred. No. 4.6e-11; Live 35; Mismatches 77;
                                                                                                                                                                           18.9%;
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Best Local Similarity
Matches 82; Conserv
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Best Local Similarity
Matches 82; Conserv
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procession: G95948

S. Frinan, T.W.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Her C; Species: Sinorhizobium meliloti
C; Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C; Accession: G95948

R; Finan, T.W.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Her Proc. Natl. Acad. Scl. U.S.A. 98, 9889-9884, 2001
A; Title: The complete sequence of the 1,663-kb pSymB megaplasmid from the N2-fixing e A; Reference number: A95842; MUID: 21396508; PMID: 11481431
A; Tatle: The complete sequence of the 1,663-kb pSymB megaplasmid from the N2-fixing e A; Resteus: preliminary
A; Wolecule type: DNA
A; Residues: 1-367 A(NBX)
A; Cross-references: GB: AL591985; PIDN: CAC49255.1; PID: 915140741; GSPDB: GN00167
A; Experimentel source: strain 1021, megaplasmid pSymB
B; Gallbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Padola, P.; Ampe, F.; Barloy-Hubl pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Jones, T.
Science 239, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, A; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-323 <TIGR>
A;Cross-references: GB:U32832; GB:L42023; NID:g1574421; PIDN:AAC23227.1; PID:g1574422
C;Superfamily: Neisseria meningitidis glycosyl transferase A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIR-FMEENSLDFSATLIE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 -ISRENRGLIATLNEGLALAKGELIARMDADDIAYPSRLSRQVALFSAEPRLALSGTGID 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 SIIMSVYN-EPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.0%; Score 271; DB 2;
33.8%; Pred. No. 2.6e-10;
tive 52; Mismatches 79.
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EDFDLFRR--IADRFPVHMIDEALVAYRIHEDSVTSKHK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity 29.09
93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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telchuronic acid biosynthesis tuaG [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: 10-10-10 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: E84107
R;Takami, H; Nakasone, K:; Takaki, Y:; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: E84107
A;Molecule type: DNA
A;Residues: 1-257 <STO>
A;Residues: 1-257 <STO>
A;Crossreferences: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07380.1; GSPDB:G
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
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A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 LNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEENSLDFSATLIELI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |:| | | | | | | |: ::| |: :|:|| | : ::|: ||: ::|| |: ::|
70 QLEKNSGPAVSRNTAIQHARGRYLAFLDSDDQWLPEKLERQLEFWQKRNVAFSFTSYKTM 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 DOKGNLVYKORESNKIYLT--NDIRKMLLNRSILAHPTWCVKKKVFDKLMGYRDLVPVED 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 -YDFAI-----RGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIYSAILQDFYKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35;
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Pred. No. 3.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 15.5%; Score 246.5; DB 2
Best Local Similarity 29.6%; Pred. No. 6.1e-09;
Matches 80; Conservative 59; Mismatches 96
| | ::: || : |
--SIAINLMRWFGADGYS 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYIDITKITNYFQEYVIK -- KRYTQQELSK 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKLSFVKSGWYFMHYVWRSLKKY----LSK 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.9%;
24.5%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: AB2092
A; Status: preliminary
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282 QEYIRL-
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. B, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Anabaena sp. Anabaena sp. Anabaena sp. Strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002 C;Accession: AG2188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA A;Rolecule type: DNA A;Residues: 1-321 <KUR>
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A;Cross-references: GB:BA000019; PIDN:BAB74761.1; PID:g17132156; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                              186 YPYAEDYKFWSEVSRLGCLANYP-----EALVKYRLHGNQTSSYYNHEQNETAKKIKREN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 LNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEENS-LDFSATLIEL 122
                                                                                                                                                                                                                                                                                   123 IDQKG-nLVYKQRESNKIY----LTNDIRKMLLNRSILAHPTWCVKKKVF--DKLMGYRD 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 ITYYLNKIGIDIKVINSVSLLEIYHVDKSNKVLKSILYEMYMSLDKYTITSLLHFIKYHL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 LNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEEN-SLDFSATLIEL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 YRDLVPVEDYDFAIRGALA-DFKIGLLNKVLLQYRLNENGISQTNKFKQYIYSAILQDFY 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SY----VEDWDWMLRIATSYDFKV--VKEALVYYRQRSNSASKNWEAMAHSFAIVIEKAF 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----KEKSY-----IDITKITNYFQEYVIKKRYTQQELSKYFELKSTPSITIR 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              228 ATASQDLOVLKNKSYGFTYLCLAWKPLQSFQKDYQKSREFCQQAVAYY-----PSLRFS 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                63
                                                             4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein alr3062 [imported] - Anabaena sp. (strain PCC 7120)
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                                                                                                                                                                                                                                                                                                                                                                                                          LVPVEDYDF----AIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIYSAILQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 -DFYKEKSYIDITKITN----SKY--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 15.8%; Score 251; DB 2; Best Local Similarity 24.6%; Pred. No. 4.2e-09; Matches 83; Conservative 85; Mismatches 103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            276 KLYICLYLYFKSPLVRRLLINDINILVLKLFGGEKQS 312
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301 ELFDLKQNLKIIKKFIRKINV 321
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Wa	Matches 78; Conservative 71; Mismatches 129; Indels 41; Gaps 13;	Db 124 MLVFDEFGVRGARILPSVPEPGIMAKGTPFCHGTIMMRAS 163
Oy Op	4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63	QY 166 VFDKLMGYRDLVPVEDYDFAIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYI 222 1 1 1
Qy Dp	64 LNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEENS-LDFSATLIEL 122	QY 223 YSAILQDFYKEKSYIDITKITNYFQEYVIKKRYTQQELSKYFELKSTPSITIRKLYICLY 282 1 Db · 210SDAFKRRSFTYSIDNAILVYQACRRL
Oy Dp	123 IDQKGNLVYKQRESNKIYLTNDIRKMLLNRSILAHPTWCVKKKVFDKLMGY-RDLVPV 179	Qy 283 LYFKSPLVRRLL 294 3 : Db 243 IYIAKPLIRAFM 254
ç a	180 EDYDFAIR-GALADFRIGLLNKVLLQYRLNENGISQTNKFKQYIYSAILQDFYKEKSYID 238 :: : : : : : 182 EDLEWILRVSSTTDWQIQGINOVLTRYRTSSSGLS-SNLYYMEAGHKQLVNRARIYAP 238	RESULT 13 A69728
ογ	ITKITNYFQEYVIKKRYTQQELSKYFELKSTPSITIRKLYICLYLYFKSPLVRRLLINDI 298	biosynthesis of teichuronic acid tuaG - Bacillus subtilis C;Species: Bacillus subtilis C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
g &	w 282	C; Accession: A69728 R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
qq	: : : 283 RLLFHOPORTFFTLLAVFG 301	A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 199. Errington, D. Spills N. S
RESULT	T 12	Achturists Fourget, D.; Filts, C.; Fuller, M.; Fuller, S.; Fulle, M.; Fuller, S.; Hullo, M.; Kotter, D.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino, M.; Kurita, M.; Kurita, K.; Lapidus, A.; Lardino, M.; Kurita, K.; Lapidus, A.; Lardino, M.; Kurita, K.; Lapidus, A.; Lardino, M.; Lapidus, A.; L
exop C; Sp(Jysaccharide biosynthesis homolog yveO - Bacillus subtilis	A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl
C; Da	e: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999 ession: D70036	A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
R; Ku	<pre>ist, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter iron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd ihrlich, S. D.; Emmerson, P. T.; Entian, K. D.; Errington, J.; Fabret, C.; Ferrari, F.</pre>	T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A;Title: The complete genience of the Gram-positive barterium Barillus subtili
Natu A: Au	e 390, 249-256, 1997 hors: Foulger, D.: Fritz, C.: Fulita, M.: Fulita, Y.: Fuma, S.: Galizzi, A.: Galler	A; Reference number: A69580; MUID: 98044033 A: Accession: A69728
Koet	J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. er, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,	A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A; Au y, M Rie	hors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueell, G. Gawa, R.; Oqiwara, A.; Oudega, B.; Park, S.H.; Partro, V.; Pohl, T.M.; Portetelle er, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,	A; Residues: 1-252 <kun> A; Cross-references: GB: 259122; GB: AL009126; NID: 92636029; PIDN: CAB15572.1; PID: e11844 A; Experimental source: strain 168</kun>
A; Au akeu T.; [hors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror. Ahl, W.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, inters, P.; Wippt, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, R.	C;Genetics: A;Gene: tuaG
A; Au A; Ti	hors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. Le: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.	Query Match 13.8%;
A; Re	ierence number: A69580; MUID:98044033 :ession: D70036; moloin and a moloin a moloin and a moloin a moloin and	Best Local Similarity 27.9%; Pred. No. 3c Matches 79; Conservative 45; Mismatche
A; Re	A. Molecule type: DNA A. Mucretc acid sequence not shown; translation not shown A. Residues: 1-278 < CKUN> A. CROSS-references: GB: 299121; GB: AL009126; NID: 92635827; PIDN: CABIS438.1; PID: e1186121;	QY 4 SIIMSVYNEPLNYVBOSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
A; Ex C; Ge A; Ge	erimental source: strain 168 netics: ne: yveO	QY 64 LNEBLIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEENSLDFSATLIELI 123
On Be	Query Match Best Local Similarity 24.7%; Pred. No. 2.9e-07; Matches 77; Conservative 53; Mismatches 96; Indels 86; Gaps 11;	Qy 124 DQKGNLVYKQRESNKIYLTNDIRKMLLNRSILA 156
oy ob	4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRI 60	QY 157 HPTWCVKKVFDKLMGYRDLVPVEDYDFAIRGALADFKIGLLNKVLLQYRLNENGISQ 214
Qy Dp	61 KILLNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEEN 111 ::	QY 215 THKFKQYIYSAILQDFYKEKSYIDITKITHYFQEYVIKKR 254 1 : : : :
ολ	112 SLDFSATLIELIDQKGNLVYKQRESNKIYLTNDIRKMLLNRSILAHPTWCVKKK 165	RESULT 14

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64 INEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEEN-SLDFSATLIEL 122
                                                                                                                                   123 IDQKGNLVYKQRESNKIYLTNDIRKMLLNRSIL---AHPTWCVKKKVFDKLMGY-RDLVP 178
                                                                                                                                                                               233 YQARPAIGNHILHLSIANLYKYLACKALQKPYSRSKGLAAVKFIWQYFLYDSS---RMRR 289
                                                                                                                                                                                                                                                                                                                         67 FSFENAGGNVSRNRGLNLAVGKFISFLDADDIWTPNKLESQLEALHNNPGFHVAYSWTDY
                                                                                                                                                                                                                                                                             179 VEDYDFAIRGALADFKIGLLNK-----VLLQYRLNENGISQTNKFKQYIYSAILQDF
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium And
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                           D.;
                  Pypothetical protein RC0461 [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Species: Rickettsia conorii
C;Species: Rickettsia conorii
C;Species: Boresoid: Soprate: 30-58p-2001
C;Species: Boresoid: Bores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
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A; Residues: 1-333 <KUR>
A; Residues: 1-333 <KUR>
A; Cross-references: GB:BA000019; PIDN:BAB73465.1; PID:g17130856; GSPDB:GN00179
A; Experimental source: strain PCC 7120
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 LNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEENSLDFSATLIELI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :::| | |:: | :| | :| | 352 FHKKNEGPAAARNLGIKNAIGKYIAFLDSDDLFYKDKIEIQLKFMEENNFIFSHTSYHKI 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DQKGNLVYKQRESNKIYLTNDIRKMLLNRSILAHPTWCVKKKVFDKLMGYRDLVPVED-- 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                469 LWISIASKNSIGGIDKELSKVRISGGTNTFMDPNKYSVGLIN--ITSYVLNDAYLSKFSP 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----DFKIGLLNKVLLQYRLNENGISQTNK 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein all1766 [imported] - Anabaena sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.8%; Score 220; DB 2; Length 60 25.8%; Pred. No. 9e-07; ive 65; Mismatches 118; Indels
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Matches 77; Conservative
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Matches 75; Conserv
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Sequence Seq

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08312387B
Patent No. 5545533
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GOLSCHLICH, EM11 C.
TITLE OF INVENTION:
GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION:
OLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 348;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/312,387B
FILING DATE: July 7, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.2%; Score 210.5; DB 1; 27.8%; Pred. No. 1.3e-11; ative 55; Mismatches 123;
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: JACKSON ESG., DAVID A.
REGISTRATION NUMBER: 26,742
REFRENCE/DOCKET NUMBER: 600-1-095
TELECOMMUNICATION INFORMATION:
TELEFAX: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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Best Local Similarity
Matches 86; Conserv
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584.496 Million cell updates/sec
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Sequence
                                                                                                                                 July 31, 2002, 18:50:29; Search time 13.08 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1: /cgg2_6/ptcdata/2/laa/5A_COMB.pep:*
2: /cgn2_6/ptcdata/2/laa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/2/laa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/2/laa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/2/laa/FCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/2/laa/FCTUS_COMB.pep:*
                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-683-426-11

US-08-683-458-11

US-08-878-360-3

US-08-878-360-11

US-08-878-140B-3

US-09-333-412-3

US-09-333-412-11

US-08-312-387B-12

US-08-683-426-5

US-08-683-426-5

US-08-683-458-12

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US-08-878-360-12

US-08-878-360-12

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US-09-333-412-5

US-09-333-412-12
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US-08-961-083-196
US-08-961-083-202
                                                                                                                                                                                                                                                                                                                                                                                  hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                              231628 segs, 24425594 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                             protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                US-09-900-038A-1
                                                                                                                                                                                                                                                                                                                                                                                                                       length: 0
length: 2000000000
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SATLIELIDQK-GNLVYKQRESNKIYLT----NDIRKMLLNRSILAHPTWCVKKKVFDKL 170
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                                                                                                                                    MGY - - - RDLVPVEDYDF - - - - AIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: GLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/683,426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 13.2%; Score 210.5; DB 1; Best Local Similarity 27.8%; Pred. No. 1.3e-11; Matches 86; Conservative 55; Mismatches 123;
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APPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: All Hackensack Avenue CITY: Hackensack Avenue CITY: Hackensack COUNTR: New Jersey ZIP: 07601
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5705367
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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TELEX: 133521
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
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....rERISTICS:
....rH: 348 antho acids
TYPE: anino acid
TOPOLOGY: 11...
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CLASSIFICATION: 536
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                         64 LNEENIGLASSLNKAV-KISK----GEYIFRMDADDISYPSRFDKQIRFMEENS--LDF 115
                                                                                      SATLIELIDQK-GNLVYKQRESNKIYLT----NDIRKMLLNRSILAHPTWCVKKKVFDKL 170
                                                                                                                                                                          171 MGY---RDLVPVEDYDF----AIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIY 223
                                                                                                                                                                                                                                                                 224 SAILQDFYKEKSYIDITKITNYFQEYVIKKRYT----QQELSKYFEL--KSTPSITIRKL 277
                                                                                                                                                                                                                                                                                                          235 -EIAQGIQK-----TARNDFLQSMGFKTRFDSLEYRQTKAAAYELPEKDLPEEDFERA 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: GOLSCHLICH, EMIL C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/312,307B
FILING DATE: JULy 7, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.2%; Score 210.5; DB 1; larity 27.8%; Pred. No. 1.3e-11; Conservative 55; Mismatches 123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/08312387B Patent No. 5545553 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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amino acid
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STATE: New Jersey
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Best Local Similarity
Matches 86; Conserv
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64 LNEENIGLASSLNKAV-KISK-----GEYIFRMDADDISYPSRFDKQIRFMEENS--LDF 115
                         64 AQAQNSGLIPSLNIGLDELAKSGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIAM 123
                                                                            116 SATLIELIDQK-GNLVYKQRESNKIYLT----NDIRKMLLNRSILAHPTWCVKKKVFDKL 170
                                                                                                        235 -EIAQGIQK------TARNDFLQSMGFKTRFDSLEYRQTKAAAYELPEKDLFEEDFERA 286
                                                                                                                                                             171 MGY----RDLVPVEDYDF----AIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIY 223
                                                                                                                                                                                                                                              SAILQDFYKEKSYIDITKITNYFQEYVIKKRYT----QQELSKYFEL--KSTPSITIRKL 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: GLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,426
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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFENCE/DOCKET NUMBER: 600-1-095B
TELECOMMUNICATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/08683426 Patent No. 5705367 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 201343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein US-08-683-426-11
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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287 RRFLYQCFK 295
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US-08-683-426-11
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224 SAILQDFYKEKSYIDITKITNYFQEYVIKKRYT----QQELSKYFEL--KSTPSITIRKL 277
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                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Gotschlich, Emil C.
APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SOUR
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.2%; Score 210.5; DB 1; 27.8%; Pred. No. 1.3e-11; ative 55; Mismatches 123;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08683458 Patent No. 5798233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 3:
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Best Local Similarity 27.8°
Matches 86; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New Jersey
COUNTRY: USA
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                                                                                                                                        278 YICLYLYFK 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07601
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US-08-683-458-3
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                                                                                        MGY---RDLVPVEDYDF----AIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIY 223
                                                                                                                                                                                                                                   235 -EIAQGIQK-----TARNDFLQSMGFKTRFDSLEYRQTKAAAYELPEKDLPEEDFERA 286
4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
                    224 SAILQDFYKEKSYIDITKITNYFQEYVIKKRYT----QQELSKYFEL--KSTPSITIRKL
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Patent No. 5798233
GENERAL INFORMATION:
APPLICANT: GOTSCHAICH, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 210.5; DB 1;
Pred. No. 1.3e-11;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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27.8%;
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3%: linear
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Best Local Similarity
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                                                                  4 SIIMSVYNEPLNYVRDSVESILLQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
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Patent No. 5945322
GENERAL INFORMATION:
APPLICANT: GOLSCHLICH, EM11 C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: GLGOSACCHARIDES, AND GENES ENCODING THEM
86; Conservative 55; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLICATION NUMBER: US/08/878,360
FILING DATE: 18-JUN-1997
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
CLASSIFICATION: 435
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411 Hackensack Avenue
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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
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TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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CORRESPONDENCE ADDRESS:
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OGY: linear
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ZIP: 07601
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SACCHARIDE UNITS WITH A POLYGLYCOSYLTRANSFERASE, POLYGLYCOSYLTRANSFERASE AND GENE ENCODING A POLYGLYCOSYLTRANSFERASE
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                                                                                                                                                                                                                                                                                                                                                                                       235 -EIAQGIQK------TARNDFLQSMGFKTRFDSLEYRQTKAAAYELPEKDLPEEDFERA 286
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                                                                                                                        Length 348;
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APPLICANT: ROTH, STEPHEN
APPLICANT: BUCZALA, STEPHANIE L.
TITLE OF INVENTION: METHOD OF TRANSFERRING AT LEAST TWO
TITLE OF INVENTION: SACCHARIDE UNITS WITH A POLYGLYCOSYL
TITLE OF INVENTION: POLYGLYCOSYLTRANSFERASE AND GENE ENG
TITLE OF INVENTION: POLYGLYCOSYLTRANSFERASE
NUMBER OF SEQUENCES: 8
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                 13.2%; Score 210.5; DB 2; 27.8%; Pred. No. 1.3e-11; iive 55; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/478,140B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08478140B; Patent No. 6127153; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (212) 790-9090
(212) 869-9741/8864
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NAME: Laura A. Coruzzi
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 714
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                 Query Match
Best Local Similarity 27.8%
Matches 86; Conservative
                                 , MOLECULE TYPE: protein US-08-878-360-11
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ZIP: 10036-2711
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                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                              171 MGY---RDLVPVEDYDF----AIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIY 223
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                                                                                                                                         Gaps
                                                                                                                 4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11. Application US/08878360
Patent No. 5945322
GENERAL INFORMATION:
APPLICANT: GCLSCALICH, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF TITLE OF INVENTION: GLIGOSACCHARIDES, AND GENES ENCODING THEM NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: All Hackensack Avenue
STREET: 411 Hackensack Avenue
                                        Length 348;
                                   13.2%; Score 210.5; DB 2; Length 27.8%; Pred. No. 1.3e-11; tive 55; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,360
FILING DATE: 18-JUN-1997
CLASSIFICATION: 435
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FILING DATE: September 26, 1994
CLASSIFICATION: 435
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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-
TELECOMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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APPLICATION NUMBER: 08/683,426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
                                                                           86; Conservative
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                                                      Similarity
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                                   Query Match
Best Local S
Matches 86
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
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COUNTRY: USA
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Best Local Similarity 27.8
Matches 86; Conservative
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US-08-478-140B-8
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                                                                                                                                                                                                                                                                                                                                                         SATLIELIDQK-GNLVYKQRESNKIYLT----NDIRKMLLNRSILAHPTWCVKKKVFDKL 170
                                                                                                                                                                                                                                                                                                                                                                                                                             MGY---RDLVPVEDYDF----AIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIY 223
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                                                                                                                                                                              Gaps
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                                                                                                                                             Length 348;
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Patent No. 6127153
GENERAL INFORMATION:
APPLICANT: JOHNSON, KARL F.
APPLICANT: ROTH, STEPHEN
APPLICANT: BOCZALA, STEPHANIE L.
TITLE OF INVENTION: METHOD OF TRANSFERRING AT LEAST TWO
                                                                                                                                                                              Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                            DB 3;
                                                                                                                                                                            55; Mismatches 123;
                                                                                                                                                          1.3e-11;
                                                                                                                                            Score 210.5;
Pred. No. 1.3
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1155 Avenue of the Americas
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FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
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NAME: Laura A. Coruzzi
REGISTRATION NUMBER: 30,742
                                                                                                                                            13.2%; 27.8%;
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
                                                                                                                                        Query Match
Best Local Similarity 27.8
Matches 86; Conservative
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                                                                     ; MOLECULE TYPE: protein US-08-478-140B-3
                                                      linear
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                                                      TOPOLOGY:
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                                                                 Gaps
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Sequence 1, Application US/09333412
Patent No. 6342382
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
                                                                 45;
         Length 348;
                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
13.2%; Score 210.5; DB 3; 27.8%; Pred. No. 1.3e-11; ive 55; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: July 7, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION UNDBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095
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FILING DATE: 15-Jun-1999
CLASSIFICATION: <UNKNOWN>
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ADDRESSEE: Klauber & Jackson
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64 LNEENIGLASSLNKAV-KISK----GEYIFRMDADDISYPSRFDKQIRFMEENS--LDF 115
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Patent No. 554553
GENERAL INFORMATION
TIPORMATION
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                               Length 348;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                         13.2%; Score 210.5; DB 4; 27.8%; Pred. No. 1.3e-11; tive 55; Mismatches 123;
                    REFERENCE/DOCKET NUMBER: 600-1-095
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPRAX: 201 343-1684
                                                                                                                                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 11: US-09-333-412-11
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July 7, 1994
  REGISTRATION NUMBER: 26,742
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                                                                                                                                                                    LENGTH: 348 amino acids
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                                                                                                    TELEX: 133521
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 86; Conserva
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Patent No. 6342382
GENERAL INFORMATION:
APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF OLIGOSACCHARIDES, AND GENES ENCODING THEM
                                                                                                                                                                                                                                                                                                   Length 348;
                                                                                                                                                                                                                                                                                                                                             Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,412
FILING DATE: 15-Jun-1999
CLASSIFICATION: <university
                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                               13.2%; Score 210.5; DB 4; 27.8%; Pred. No. 1.3e-11; tive 55; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/312,387
FILING DATE: July 7, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
                                                                                                                                                                TOPOLOGY: 11near
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
FELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
                 TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                        LENGTH: 348 amino acids TYPE: amino acid
                                                                           INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS
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                                                         TELEX: 133521
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Matches 86; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-333-412-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: GOLSCHLich, Emil C.

TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF

TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM

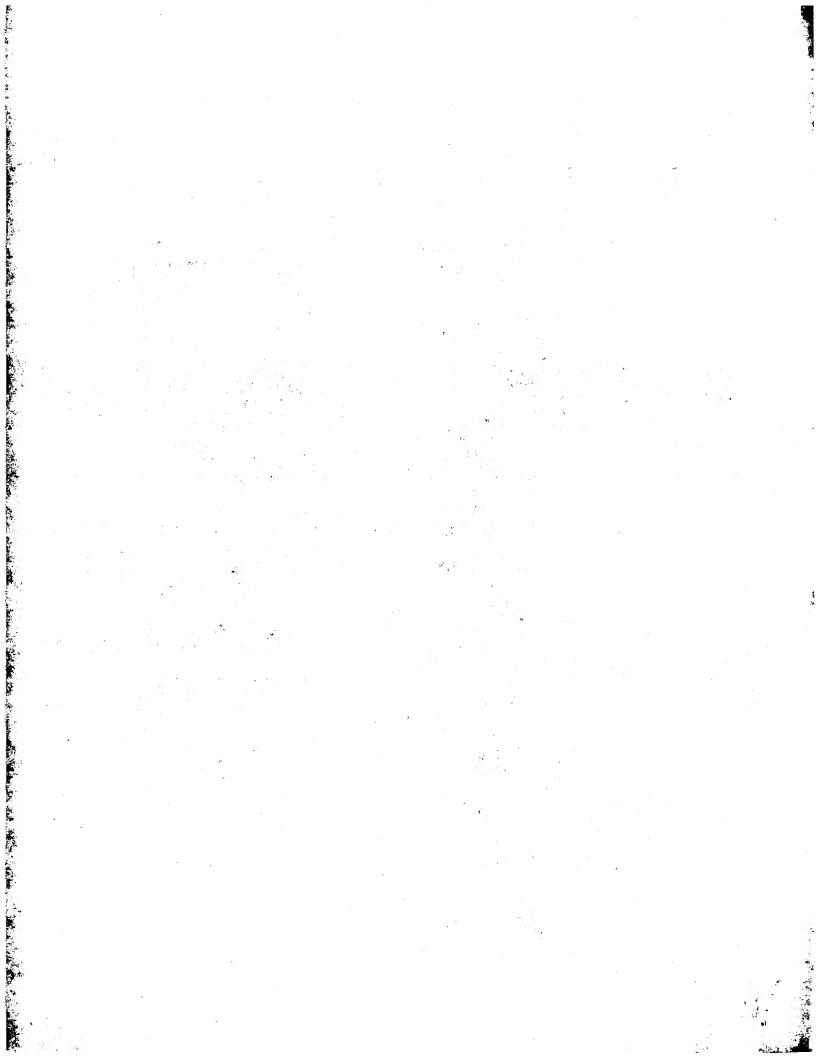
NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson
                                                                                                                                                                              Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,426
                                                                                                                                                                              DB 1;
                                                                                                                                                                         11.1%; Score 176.5; DB 1
22.6%; Pred. No. 1.6e-08;
Live 60; Mismatches 93
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REGISTRATION NUMBER: 26,742
REFERNCE/DOCKET NUMBER: 600-1-095B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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CLASSIFICATION: 536
PLIOR PEPLICATION DATA:
APPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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411 Hackensack Avenue
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
: 337 amino acids
amino acid
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                                              TOPOLOGY: linear MOLECULE TYPE: protein
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13;
                                                                                                                                                                                                                                                                                                      177 VPVEDYDFAIRGALADFKIGLLNKVLLQYRLNENGISQTNKF·KQYIYSAILQDFYKEKS 235
                                                                                                                                                                                           64 LNEENIGLASSLN----KAVKISKGEYIFRMDADDISYPSRFDKQIRFME-ENSLDFSAT 118
                                                                                                                                                                                                             119 LIELIDQKGNLVYKQRESNKIYLTNDIRKMLLNRSILAHPTWCVKKK--VFDKLMGYRDL 176
                                                                                                                                                                                                                                                                    Query Match 11.1%; Score 176.5; DB 1; Length 337; Best Local Similarity 22.6%; Pred. No. 1.6e-08; Matches 62; Conservative 60; Mismatches 93; Indels 59; Gaps
                                                                                                                                                       4 SIIMSVYNEPLNYNBOSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
                                                                                                                                                                                                                                                                                                                                                             ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-683-426-5
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Search completed: July 31, 2002, 18:56:22 Job time: 353 sec



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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein – protein search, using sw model

July 31, 2002, 18:50:19 ; Search time 30.44 Seconds (without alignments) 1142.119 Million cell updates/sec Run on:

US-09-900-038A-1

Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 747574 seqs, 111073796 residues Searched:

747574

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

•• Database

A_Geneseq_032802:*

/SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/Aa1980.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/Aa1981.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/Aa1981.DAT:*
/SIDSI/gcgdata/hold-geneseqy/geneseqp-emb1/Aa1983.DAT:*
/SIDSI/gcgdata/hold-geneseqy/geneseqp-emb1/Aa1984.DAT:*
/SIDSI/gcgdata/hold-geneseqy/geneseqp-emb1/Aa1985.DAT:*
/SIDSI/gcgdata/hold-geneseqy/geneseqp-emb1/Aa1985.DAT:*
/SIDSI/gcgdata/hold-geneseqy/geneseqp-emb1/Aa1986.DAT:*
/SIDSI/gcgdata/hold-geneseqy/geneseqp-emb1/Aa1987.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Enzyme EPSH involv	Amino acid sequenc	C qlutamicum prote	Campylobacter jeju	Amino acid sequenc	Enterococcus faeca	Enterococcus faeca	Cps9G protein whic	Sugar transferase	N. gonorrhoeae gly	Neisseria polyglyc
SUMMARIES	AAY 54 093	AAY43795	AAG90151	AAY97206	AAY68985	AAU33454	AAU34918	AAY68980	AAW88312	AAR91311	AAW06576
DB	21	21	22	21	21	22	22	21	20	17	18
% Query Match Length DB	268	268	274	301	209	706	715	569	260	348	348
% Query Match	17.1	17.1	15.1	14.7	14.0	13.6	13.6	13.5	13.4	13.2	13.2
Score	272	272	240.5	234	223	216	216	214	213	210.5	210.5
Result No.	-	7	m	4	S	9	7	80	σ	10	11

Cpsli protein whic Campylobacter jeju Putative glycosylt Enzyme EPSJ involv Amino acid sequenc Cps2J protein whic	C glutamicum prote EpsM. Lactococcus Campylobacter jeju N. gonorrhoeae gly Lipo-oligosacchari S premimoniae gly	P. multocida hyalu Pasteurella multoc P. multocida hyalu CpsZK protein whic Enzyme EPSM involv Amino acid sequenc		Enzyme Erso involve Amino acid sequecn CpslJ protein which Enzyme Ersy which Amino acid sequence Novel human diagno Novel human diagno Novel human diagno Novel human diagno Enzyme EPS8 which
AAY68974 AAY97203 AAB96313 AAY54095 AAY43797 AAX68962	AAG90140 AAB47427 AAY97213 AAR91314 AAW06579	AAY96212 AAY06212 AAY43099 AAY68963 AAY54098 AAY4631	AAY689513 AAY68976 AAW14078 AAW22177 AAY81720 AAW61236 AAW61236	AAY 44080 AAY 482 AAY 68972 AAY 54071 ABC 2248 ABC 13176 ABC 25145 AAY 54072
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12 13 14 15 17	18 20 22 23	2400000 400000	, w w w w w w w w w w w w w w w w w w w	0 6 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

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RESULT

AAY54093

AA. AAY54093 standard; Protein; 268 (first entry) 27-MAR-2000 AAY54093;

Enzyme EPSH involved in exopolysaccharide blosynthesis.

Exopolysaccharide; EPS; ESP enzyme; EPSA; EPSB; EPSB; EPSD; EPSF; EPSG; EPSH; EPSJ; EPSJ; EPSK; Lactobacillus delbrueckii buigaricus; activated D-galactose pyranose; saccharide, beta-glycosyltransferase; transcription attenuator; glucosyl-phospho-transferase; alpha-glycosyltransferase; glucosyltransferase; EPSL; EPSM; alpha-glycosyltransferase; EPS Dolymerase; glycosyltransferase; EPS polymerase; glycosyltransferase; EPSN; phosphofuranose; transporter; food; fermented milk product; yoghurt; cheese; flavour stability; organoleptic property. THE STATE OF THE S

Lactobacillus delbrueckii bulgaricus.

WO9962316-A2

22-APR-1999; 09-DEC-1999

99WO-EP02841.

98EP-0201310. 98EP-0201311. 98EP-0201312. 22-APR-1998; 22-APR-1998; 22-APR-1998;

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Germond JE, Lamothe G; Stingele F, ~

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                                                                                                                                                                                                                                                                                          exopolysaccharides (ERS). These energyes are designated EPSA-EPSN, and are encoded by open reading frames epsA-epsN. The enzymes are isolated from Lactobacillus delbrueckii bulgaricus. The proteins are used in a method for the synthesis of EPS, which includes at least one step of forming a bond (alpha or beta-isomer) between C-1 (carrying the reducing aldebyde function, of an activated D-galactose pyranose), and a phosphate on a lipophilic or proteinaceous primer. Stepwise synthesis of EPS occurs with, in each step, addition of a new sugar unit, through its hemi-acetyl function, to an alcoholic hydroxyl of a second sugar unit, present at the end of a chain of sugar residues bonded to the primer. EPSA is attenuator of transcription which influences for involved in the control of the molecular weight and/or the length of the could play saccharide; EPSD, EPSL and EPSM are involved in synthesis of EPS in involved in the first saccharide on the primer; EPSF and EPSR are involved in synthesis of the captage of placosyl-phospho-transferase which catalyses the transfer of the first saccharide on the primer; EPSF and EPSR is capha-glucosyltransferases; EPSG as a glucosyltransferase; EPSG is a glucosyltransferase; EPSK is capha-glucosyltransferases; EPSG is a glucosyltransferase; EPSK is cresponsible for the polymerisation of the repetitive units; and EPSN is responsible for export of the EPS. The EPS enzyme are used to improve properties of foods, particularly fermented milk products such as yophurt and cheese, e.g. their organoleptic properties and flavour stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 IELIDQKGNLVY ---KQRESNKIYLINDIRKMLLNRSILAHPTWCVKKKVFDKLMGYR-- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:|||:|| || : |:|||::|| :||| | : | ::| : |:|| | ::| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 SIIMSVYNEPLNY--VRDSVESILNQTLTDFEFIIVID-NPSRGDLKQFLTEYSVVDNRI 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 -DLVPVEDYDFAIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIYSAILQDFYKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36;
                                                                                 new recombinant enzymes for synthesis of exopolysaccharides, particularly in lactic acid bacteria, for improving properties fermented milk products
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                                                                                                                                                                                                                                                                         AAY54086-99 represent enzymes involved in the biosynthesis of
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Pred. No. 5.3e-17;
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                                                                                                                                                                                                                    Claim 13; Page 154-155; 162pp; French
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29.7%;
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                         2000-097267/08.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 AA;
                                                     N-PSDB; AAZ54260
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by the eps operon of Lactobacillus delbrueckii bulgaricus Lifs. The oper no contains 14 open reading frames, and encodes enzymes (epsA, epsC, epsD, epsE, epsE, epsE, epsE, and encodes enzymes (epsA, epsE,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
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epsB; epsC; epsB; epsE; epsE; epsB; epsH; epsI; epsK; epsE; epsM; exopolysaccharide biosynthesis; EpS; intersugar bond; antitumour; probiotic; foodstuff; organoleptic quality; flavour; lactic acid bacteria; acidified milk product; yoghurt; cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New recombinant enzymes for biosynthesis of exopolysaccharides having e.g. antitumor or probiotic properties or useful in fermented milk
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Pred. No. 5.3e-17;
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                                                                                                                                                                                                                                           Lactobacillus delbrueckii bulgaricus
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98EP-0201312.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-013255/01
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ30357
                                                                                                                                                                                                                                                                                                                                          W09954475-A2
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22-APR-1998;
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products
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188

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AAY97206

130 if---gqsadlptsqdirqillvknpiihssvmyrkqvveqiggyslemtrsqdyelflr 186 ----GALADFKIGLLNKVLLQYRLNENGIS-QTNKFKQYIYSAILQDFYKEKSYIDITKI 242

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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ochiai K, Yokoi H;
                                                                                                                                                                                                                                                                                      Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 17; SEQ ID NO: 3905; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S, Hayashi M,
Ozaki A;
                                                                                                                                                                                                                          C glutamicum protein fragment SEQ ID NO: 3905
                                 AAG90151 standard; Protein; 274 AA.
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26.2%; Pred
arive 72; M
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2000JP-0159162.
2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-DEC-2000; 2000EP-0127688.
                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium glutamicum.
                                                                                                                                                           (first entry)
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07-APR-2000;
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Tatelshi N,
                                                                                                                                                           26-SEP-2001
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                                                                                                AAG90151;
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AAG90151
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are useful for synthesising simplates of a staryment of staryment of staryments of staryments of oligosaccharides useful for chemo-enzymatic synthesis of oligosaccharides, are useful for chemo-enzymatic synthesis of oligosaccharides, including gangliosides and other oligosaccharides that have biological activity. The enzymes and nucleic acids that encode them are useful for studies of the pathogenesis mechanisms of organisms that synthesize ganglioside mimics, such as C. jejuni and the nucleic acids are used as probes to study expression of genes involved in ganglioside mimetic synthesis. Antibodies raised against the glycosyltransferases are also useful for analyzing the expression patterns of these genes involved in pathogenesis. The nucleic acids are also useful for designing antisense oligonucleotides for inhibiting expression of the Campylobacter cancer are involved in the biosynthesis of ganglioside mimics that can mask the pathogens from the host's immune system. The oligosaccharides are useful as diagnosing reagents or as therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel glycosyltransferase polypeptides and polynucleotides useful for biosynthesis of ganglioside and ganglioside mimics, as diagnostic reagents and as immunogen for producing antibodies
                                                                                                                                                                                       acetyltransferase; glycosyltransferase; Beta-1,4-GalNAc transferase; Beta-1,3-galactosyltransferase; alpha-2,3-sialyltransferase; sialic acid synthase; CMP-sialic acid synthetase; mimic; antibody; immunogen; ganglioside.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A reaction mixture for the synthesis of a sialylated oligosaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and as immunogens for producing antibodies. Bacterial glycosyltransferase can be used to catalyse the formation of oligosaccharides that are identical to the corresponding mammalian structures and are easier and less expensive to produce in large quantity, compared to the mammalian glycosyltransferase. The
                                                                                                                              Campylobacter jejuni OH4384 Beta-1,3-galactosyltransferase.
                                                                                                                                                                        Biosynthetic locus; biosynthesis; lipid A biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 13; Page 102-103; 120pp; English.
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AAY97206 standard; Protein; 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CANA ) NAT RES COUNCIL CANADA.
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31-JAN-2000; 2000US-0495406.
                                                                                                                                                                                                                                                                                                      Campylobacter jejuni OH4384.
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                                                                                    (first entry)
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                                                                                    22-DEC-2000
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                                          AAY97206;
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10;

Gaps

27;

Length 274;

Score 240.5; DB 22; Length Pred. No. 4.5e-14; 2; Mismatches 101; Indels

Conservative Similarity

Local Sim.

Best Loc Matches

Query Match

129 LVYKQRESNKIYLTNDIRKMLLNRSILAHPTWCVKKKVFDKLMGYR-DLVPVEDYDFAIR 187

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70 GLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEENS-LDFSATLIELIDQKGN 128

YNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKILLNEENI 69

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Disclosure; Fig 6; 144pp; English.

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13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid containing the capsular gene cluster of Streptococcus suis, used for serotype-specific detection and to generate antigens or mutants for vaccination \,
                                                                                                                                                                                                                                                                                 DQKGNLVYKQRESNK-IYLTNDIRKMLLNRSILAHPTW--CVKKKVFDKLMGYRDLVPVE 180
                                                                                                                                                                                                                                                                                                     181 DYDFAIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIYSAILQDFYKEKSYIDIT 240
                                                                                                                                                                                                                                                                                                                                                                 172 ---fas1rlekdvkinmaedvilyypm----lsqaqkia--ymncnlyhyvpnnnsicnt 222
                                                                                                                                                                                                                                                                                                                                                                                                                    LNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEENSLDFSATLIELI 123
                                                                                                                                                                                                                                       K----ITNYFQEYVIKKRYTQQE--LSKYFELKSTPSITIR-KLYICLYLYFKSPLVRRL 293
                                                                                                                                  Gaps
                                                                                                                                                                               ||||: || ||: ::|| ::|| | ||||:|: : ||| | |||||: ||: siilptynve-qyiaraiescinqtfkdie-iivvddcgndnsiniakeyskkdkrikii 62
                                                                                                                                                              4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Capsular gene cluster; serotype 7; polysaccharide biosynthesis; capsular component; antigen; regulation; chain length determination; complement-mediated opsonophagocytosis; serotype-specific detection; antigen; vaccine; Streptococcal disease; Cps7E; Cps7E; Cps7G;
bacterial origin of the enzymes facilitates expression of large quantities of the enzymes using relatively inexpensive prokaryotic
                                                                                                                                  36;
                                                                                                     Length 301;
                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of Cps7H of a capsular gene cluster.
                                                                                                   14.7%; Score 234; DB 21; 28.2%; Pred. No. 2.1e-13; ive 53; Mismatches 135;
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                                                                                                                   Similarity 28.2'88; Conservative
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                              expression systems.
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                                                          301 AA;
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                                                                                          The proteins AAY68982-85 are encoded by the capsular gene cluster of Streptococcus suis serotype 7. The genes in this cluster are involved in polysacoharide biosynthesis of capsular components and antigens. The capsule confers bacterium resistance to complement-mediated opsonophagocytosis. The gene cluster is used as a source of probes and primers for serotype-specific detection of S. suis and is also useful for recombinant production of the proteins. The proteins are then useful for producing antigens that can be used in vaccines, for controlling or eradicating a Streptococcal disease, in humans or animals, e.g. against S. suis in pigs.
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Pred. No. 1.3e-12;
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N-PSDB; AAS51313.
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Best Local Similarity
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16-FEB-2001;
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                                                                         The Invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are scherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
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             New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibloitics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruqinosa and Enterococcus facealis. The invention is also useful for the identification of potential new targets in antibiotic development. The antisense nucleic acids can also be used to dentify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins.

The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in essential prokaryotic cellular proliferation protein.

Which is a sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 LNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEEN-SLDFSATLIEL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 freqnghiseatnsalaiatgefvalldnddelainafyevvkvlnenpeldliysdedk 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ydlvlrftekttkerithipkvlyywrmlptstavdggskgyafeaglravgdalvrrg1 417
                                                                                                                                                                                                                                                                                                                                                                                                                     Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----SYIDITKITNYFOEYVIKKRYTQOELS 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDQKGNLVYKQRESNKIYLTNDIRKMLLNRSILAHPTWCVKKKVFDKLMGYR-DLVPVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                 Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 715;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 YDFAIRGALADFK--IGLLNKVLLQYRLNENGISQTNKFKQYIYSA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.6%; Score 216; DB 22;
23.3%; Pred. No. 3.3e-11;
tive 64; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                 Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Seq ID No 10511; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                              Ohlsen KL, Zyskind JW,
Xu HH;
                                                                                                                                 2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from WIPO at
21-MAR-2001; 2001WO-US09180
                                                                                                                                                                                                                                                                         2001US-269308P
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                                                                                                                                                                                                                                                                                                                                             (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-611495/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       715 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAS52777.
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| ; ; | ;:| ;:| ;:| ; fmlaggiv-----tpldvfingiyirvfvympt- 256
                              idie--ideflustseiv----shknvptqhdeilkmarreksmchmtvmfkkksvera 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoded by the wbdN open reading frame of a gene cluster (see AxCoff49) involved in the biosynthesis of the Escherichia coli 0157 o antigen. The use of nucleic acid molecules derived from particular assembly and transport genes, particularly wbd (transferase), wax (flippase) and way (polymerase) genes, within o antigen gene clusters improves the specificity of methods for the detection and identification of 0 antigens, e.g. in testing foodor facecal-derived samples, or samples from patients. The O antigen is a major virulence factor of enteropathogenic E. coli strains that cause diarrhoea and haemorrhagic colitis.
   LDFSATLIELIDQKGNLVYKQRESNKIYLT - - NDIRKMLLNRSILAHPTWCVKKKVFDKL
                                                                                                  170 ggyqtlpyvedyflwvrmiasgskfanidetlvlarvg-ngmfnrrgnreginswtllie
                                                                    MGYRDLVPVEDYDFAIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIYS-AILQD
                                                                                                                                    FYKEKSYIDITKITNYFQEYVIKKRYTQQELSKYFELKSTP-SITIRKLYICLYLYFKSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid molecules specific for bacterial polysaccharide antigens - useful for detecting specific strains in, e.g. food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is the amino acid sequence of a sugar transferase that is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Sugar transferase involved in 0157 antigen biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     antigen; 0157 antigen; sugar transferase; wbdN gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.4%; Score 213; DB 20;
llarity 27.2%; Pred. No. 1.5e-11;
Conservative 54; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      haemorrhagic colitis; diagnosis
                                                                                                                                                                                                                                                                                                                     AAW88312 standard; Protein; 260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 8; 165pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-AU00315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97AU-0008162.
97AU-0006545.
                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-059669/05.
                                                                                                                                                                                                      289 LVRRLLINDI 298
                                                                                                                                                                                                                                     257 wikkliygki 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAX06749.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-NOV-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diarrhoea;
                                                                                                                                                                                                                                                                                                                                                      AAW88312;
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                                117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The proteins AAY68977-81 are encoded by the capsular gene cluster of Streptococcus suis serctype 9. The genes in this cluster are involved in polysaccharide biosynthesis of capsular components and antigens. The proteins have glycosyltransferase activities (Cps9E, Cps9F) and unknown functions (Cps9D, CpsG, Cps9H). The capsule confers bacterium resistance to complement-mediated opsonophagocytosis. The gene cluster is used as a source of probes and primers for serotype-specific detection of S. suis and is also useful for recombinant production of the proteins. The proteins are then useful for producing antigens that can be used in vaccines, for controlling or eradicating a Streptococcal disease, in humans or animals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid containing the capsular gene cluster of Streptococcus suis, used for serotype-specific detection and to generate antigens or mutants for vaccination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKILLNEENIGLASSLNKAVKISKGE----YIFRMDADDISYPSRFDKQIRFMEEN-S 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Capsular gene cluster; serotype 9; polysaccharide biosynthesis; capsular component; antigen; regulation; chain length determination; complement-mediated opsonophagocytosis; serotype-specific detection; antigen; vaccine; Streptococcal disease; Cps9D; Cps9E; Cps9F; Cps9G; CpsPH; glycosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNYSIIMSVY-NEPLNYVRDSVESIL-NQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 269;
                      DIEN-) STICHTING DIENST LANDBOUWKUNDIG ONDERZOE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.5%; Score 214; DB 21; 25.5%; Pred. No. 1.2e-11; ive 63; Mismatches 112;
262 KYFELKSTPSITIRKLYICLYLYFKSPLVRRLLINDINI 300
                                                                                                                                                                                                                   Cps9G protein which has an unknown function.
                                                                                                                 AAY68980 standard; Protein; 269 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 5; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-NL00460
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                                                                                                                                                                                 30-MAY-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-195104/17.
                                                                                                                                                                                                                                                                                                                                                    Streptococcus suis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 AA;
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                                                                                                                                                                                                                                                                                                                                                                                  WO200005378-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                    03-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith HE;
                                                                                                                                                  AAY68980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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Length 348;

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AAW06576;
Query Match
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Matches
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                                                                                                                                      |: |:|| | | :::: |:|| |||||: : ::|| : :| : :| 65 rnktnlgvaesrnygiematgkyisfcdaddlwhekklergievlnnecvdvvcsnyyvi 124
                                                                                                                                                                                                                             237
                                                                                                                                                                                                                                                                                                                        DQKGNLVYKQRESNKIYLTNDIRKMLLNRSILAHPTWCVKK----KVFDKLMGYRDLVPV 179
                                                                                                         LNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEENSLDFSATLIELI 123
                   63
                                                            64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 Glycosyltransferases (AAR91311-15) are products of the lgt locus (AAT44061) of Neiserria gonorrhoeae strain F62. Glycosyltransferase LgtA (AAR91311) can be obtd. by expression of the lgtA coding sequence in recombinant host cells. A method for adding GalNAc or GloNAc betal-3 to Gal comprises contacting a reaction mixture contg. activated GalNAc or GloNac to an acceptor moiety comprising a Gal residue in the presence of LgtA. Oligosaccharides can be produced that, when attached to non-toxic lipids, are useful for Neisserla waccine prepn. Blood group core oligosaccharides, and mimics of lacto-N-neotetranse, gangliosides and saccharides, and globoglycolipids can also be produced using the enzymes.
                                           180 EDYDFAIRGALADFKIGLLNKVLLQYRLNENGISQTNKFK--QYIYSAILQDFYKEKSYI
                   SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding glycosyl transferase(s) - used in the diagnosis of infection with Nelsseria and for the blosynthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycosyltransferase; lipo-oligosaccharide; lgt gene; LOS locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N. gonorrhoeae glycosyltransferase LgtA.
                                                                                                                                                                                                                                                                                                                                                                                         238 DITKITNYFQEYV -- - IKKRYTQQELSK 262
                                                                                                                                                                                                                                                                                                                                                                                                                                    228 sfpktlyyfllyasngvmkkithsllrr 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria gonorrhoeae strain F62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR91311 standard; Protein; 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; Fig 2b; 81pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-200924/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oligo:saccharide(s)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gotschlich EC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9610086-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-SEP-1994;
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15;
                                                                                                                                                SATLIELIDQK-GNLVYKQRESNKIYLT----NDIRKMLLNRSILAHPTWCVKKKVFDKL 170
                                                                                                                                                                                                                    64 LNEENIGLASSLNKAV-KISK----GEYIFRMDADDISYPSRFDKQIRFMEENS--LDF 115
                                                                                                                                                                                                                                                               MGY----RDLVPVEDYDF----AIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIY 223
                                                                                                                                                                                                                                                                              Gaps
                                                                                 4 SIIMSVYNEPLNYVRDSVESILNOTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transfer of at least 2 saccharide units using poly:glycosyl:transferase - isolated from N. gonorrhoeae, catalyses the addition of both GlcNac and GalNac di:saccharide(s) units to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A novel polyglycosyltransferase (PGTase) (AAW06576) from Neisseria gonorrhoeae ATCC 33084 catalyses the stereospecific conjugation of 2 specific activated saccharide units (e.g. UDP-GICNAC, UDP-GAINAC, UDP-GAI) to specific acceptors having a galactose moiety at a non-reducing end. It is the first PGTase reported to be capable of transfer of more than one different saccharide moiety. The PGTase is encoded by nucleotides 445-1488 of a lipo-oligosaccharide gene
                                                                                                                                                                                                                                                                                                                             SAILQDFYKEKSYIDITKITNYFQEYVIKKRYT ---- QQELSKYFEL -- KSTPSITIRKL
                                  45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polyglycosyltransferase; N-acetylglucosaminyl transferase; N-acetylgalactosaminyl transferase; lipo-oligosaccharide.
               3.8e-11
                                Mismatches
13.2%; Score 210.5; 27.8%; Pred. No. 3.86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW06576 standard; Protein; 348 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria polyglycosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roth S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria gonorrhoeae ATCC 33084
                              55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NEOS-) NEOSE TECHNOLOGIES INC.
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                                Conservative
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               Similarity
                                                                                                                                                                                                                                                                                                                                                                                              278 YICLYLYFK 286
                                                                                                                                                                                                                                                                                                                                                                                                                             287 rrflyqcfk 295
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Disclosure; Fig 4; 144pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    It can be produced in transformed host cells and used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 LNEENIGLASSLNKAV-KISK-----GEYIFRMDADDISYPSRFDKQIRFMEENS--LDF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SATLIELIDQK-GNLVYKQRESNKIYLT----NDIRKMLLNRSILAHPTWCVKKKVFDKL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 MGY---RDLVPVEDYDF----AIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIY 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235 -eiaggigk-----tarndflgsmgfktrfdsleyrgtkaaayelpekdlpeedfera 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :| || || : :::| |||| | |||||: : :|: : :||: : :||: : : :||:: : :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:: :||:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45;
                                                                                                                                                                                                                                                                                                                                                       Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55; Mismatches 123; Indels
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                                                                                                                                                                                                                                                                                                                                                 Score 210.5; DB 1 Pred. No. 3.8e-11;
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                                                                                                                                                                                                                                                                                                                                     13.2%; 27.8%;
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98EP-0202467.
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                                                       oligosaccharide prodn.
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Best Local Similarity
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The proteins AAY68970-76 are encoded by the capsular gene cluster of Streptococcus suis serotype 1. The genes in this cluster are involved in polysaccharide biosynthesis of capsular components and antigens. The proteins have glycosyltransferase activities (CpsIE, CpsIG, CpsII, CpsIJ, CpsII, and CP polymerase activities (CpsIH). The capsule confers bacterium resistance to complement mediated opsonophagocytosis. The serotype-specific detection of S. suis and is also useful for recombinant production of S. suis and is also useful for recombinant production of the proteins. The proteins are then useful for producting a Streptococcal disease, in humans or animals, e.g. suis in pigs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                               is useful for synthesising simplified oligosaccharide such as grantloside, lysoganglioside or their mimics. Glycosyltransferases are useful for chemo-enzymatic synthesis of oligosaccharides, concluding gangliosides and other oligosaccharides that have biological activity. The enzymes and nucleic acids that encode them are useful for studies of the pathogenesis mechanisms of organisms that synthesize ganglioside mimics, such as C. jejuni and the nucleic acids are used as probes to study expression of genes involved in ganglioside mimics, such as C. jejuni and the nucleic acids are used as probes to study expression of genes involved in ganglioside mimics, such as C. jejuni and the cupted sign patterns of these genes involved in pathogenesis. The culticactide are also useful for designing antisense oligonucleotides for inhibiting expression of the Campylobacter contact acids are also useful for designing antisense oligonucleotides for inhibiting expression of the Campylobacter cargines that are involved in the biosynthesis of ganglioside mimics that can mask the pathogens from the host's immune system. The oligosaccharides are useful as diagnosing pageance are useful as diagnosing pageance.
                                                                                                                       Novel glycosyltransferase polypeptides and polynucleotides useful for blosynthesis of ganglioside and ganglioside mimics, as diagnostic reagents and as immunogen for producing antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 LIDQKGNLVYKQRESNKIYLTNDIRKMLLNRSILAHPTW--CVKK----KVFDKLMGYRD 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVPVEDYDFAIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIYSAILQDFYKEKS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 lnygedvlícyiyfmfcekiavfktciyhyefnpng-ryenknkeiln----qnyhdkkk 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 LNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEE--NSLDFSATLIE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reaction mixture for the synthesis of a sialylated oligosaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIIMSVYNEPLNYVRDSVESILNOTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and as immunoses are useful as diagnosing reagents or as therapeuti and as immunogens for producing antibodies. Bacterial glycosyltransferase can be used to catalyse the formation of oligosaccharides that are identical to the corresponding mammalian structures and are easier and less expensive to produce in large quantity, compared to the mammalian glycosyltransferase. The bacterial origin of the enzymes facilitates expression of large expression systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.6%; Score 200; DB 21; Length 270; 26.8%; Pred. No. 2.5e-10; Live 52; Mismatches 119; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 YIDITKITNYFQEYVIKKRYTQQEL-SKYFEL 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 115-116; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB96313 standard; Protein; 298 AA
              (CANA ) NAT RES COUNCIL CANADA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                             Gilbert M, Wakarchuk WW;
                                                                         WPI; 2000-524418/47.
N-PSDB; AAA53720.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S:
Matches 73,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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The present invention relates to the genomic sequence of Pyrococcus abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi is a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to 110 degrees centigrade.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 LIDQKGNLVYKQRESNKIYLTNDIRKMLLNRSILAHPTWCVKKKVFDKLMGYRD--LVPV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 LNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEENSLDFSATL--IE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 yvsqdgrilgkrlpkhr----gdiyshllkenfigsptllirrecfkk-aglfdprlsss 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAG66436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
                                                         Putative glycosyltransferase, involved in cell wall biogenesis #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleotide sequences isolated from Pyrococcus abyssi encode proteins useful in industry -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lecompte
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                                                                                                               Hyperthermophilic archaeon; hyperthermophilic protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Forterre P, Thierry JC, Prieur D, Dietrich J, I
Querellou J, Weissenbach J, Saurin W, Heilig R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 198; DB 22;
Pred. No. 4.3e-10;
0; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Pages 981-982; 1657pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
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27.8%;
                                                                                                                                                                                                                                                                                                                                           99FR-0005034.
                                                                                                                                                                                                                                                                                                                                                                                                     99FR-0005034.
29-OCT-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-126236/14.
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Best Local Similarity
Matches 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 AA;
                                                                                                                                                                        Pyrococcus abyssi
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                                                                                                                                                                                                                            FR2792651-A1
                                                                                                                                                                                                                                                                                                                                              21-APR-1999;
                                                                                                                                                                                                                                                                                     27-OCT-2000.
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Page 10

ESP enzyme; EPSA; EPSB; EPSB; EPSD; EPSE; EPSF;

us-09-900-038a-1.rag

Lamothe G;

AAY54086-99 represent enzymes involved in the biosynthesis of exopolysaccharides (EBS). These enzymes are designated EPSA-EPSN, and are encoded by open reading frames epsa-epsN. The enzymes are isolated from Lactobacillus delbrueckii bulgarius. The proteins are used of from ing a bond (alpha or beta-isomer) between C-1 (carrying the reducing aldehyde function, of an activated D-galactose pyranose), and a phosphate on a lipophilic or proteinaceous primer. Stepwise synthesis of ESS occurs with, in each step, addition of a new sugar unit, through its hami-acetyl function, to an alcoholic hydroxyl of a second sugar unit, present at the end of a chain of sugar residues bonded to the primer. EPSA is attenuator of transcription which influences primer. EPSA is attenuator of transcription which influences regulation; EPSB determines the length of the saccharide chain; EPSC is involved in the control of the molecular weight and/or the length of the polysaccharide; EPSD, EPSL and EPSM are involved in Synthesis of EPSL; encoding and EPSM are involved in Synthesis of EPSL; encoding and EPSM are involved in Synthesis of EPSL; encoding and EPSM are involved in Synthesis of EPSL; encoding and EPSM are involved in Synthesis of EPSL; encoding and EPSM are involved in Synthesis of EPSL; encoding and EPSM are involved in Synthesis of EPSL; encoding and EPSM are involved in Synthesis of EPSL; encoding and EPSM are involved in Synthesis of EPSL; encoding and EPSM are involved in Synthesis of EPSL; encoding and EPSM are involved in Synthesis of EPSL; encoding and EPSM are involved in Synthesis of EPSL; encoding and EPSM are involved in Synthesis of EPSL; encoding and EPSM are involved in Synthesis of EPSL; encoding and EPSM are involved in Synthesis of EPSL; encoding and EPSM are involved in Synthesis of EPSL; encoding and EPSM are involved in Synthesis of EPSL; encoding and EPSM are involved in Synthesis of EPSL; encoding and EPSM are involved in Synthesis of EPSL; encoding and EPSM are involved and Synthesis of EPSL; encoding and EPSE is a glactosy or glucosyl-phospho-transferase which catalyses the transfer of the first saccharide on the primer: EPSF and EPSG are alpha-glycosyltransferases; EPSG is a glucosyltransferase; EPSG is a glucosyltransferase; EPSK is responsible for the polymerisation of the repetitive units; and EPSN is responsible for export of the EPS. The EPS enzyme are used to improve properties of foods, particularly fermented milk products such as yoquurt ond cheese, e.g. their organoleptic properties and flavour stability. New recombinant enzymes for synthesis of exopolysaccharides, particularly in lactic acid bacteria, for improving properties of Example 18; Page 156-157; 162pp; French fermented milk products 327 AA; Sequence

15; Gaps 1 MNYSIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRI 60 73; DB 21; Length 327; Indels 121; 12.2%; Score 193.5; DB 27.25.0%; Pred. No. 1.3e-09; Mismatches 55; Conservative Similarity 83; Query Match Best Local Si Matches 83) ò

61 KILLNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEENSLDFSATLI 120

> g δy

121 ELIDQKGNLVYKQRESNKIYLTNDIRK--MLLNRSILAHPTWCVKKKVFDKLMGYRDLVP 178 ggsithtsstvnydamyasrevydfvkkrqpeytaeanfayvfsrigvidnltvqptvdk 269 234 59 kv-vhkqngglssarnagmkvatgeyisfidsddylasnmyehvfsimkkecadivvvgr 117 179 VEDYDFAIRGALADFKIGLLNKVLL-QYRLNENGISOTNKF---KQYIYSAILQDFYKEK --SYIDITKITNYFQEYV-----IKKR---YTQQELSKYF-----ELKSTPSITI 160 wdkv-----ykrslfndvsypegklsedwyttykvfakanrivydstpmyyyrgr 287 RKLYICLYLYFKSPLVRRLLINDI -- NILVLK 304 | : ||: || || ----rkirndmkanikqlk qki----275 118 235 210 270 g q δ g ŏ ö ò

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